

XX Activin receptor; activin/TGF-superfamily; receptor protein; function;  
KW activity; modulate; treatment; carcinogenesis; wound healing; fertility;  
KW immune system disorder; central nervous system disorder; human;  
KW reproductive system.  
KW

DR N-PSDB; AAX22685.

XX Isolated nucleic acid molecules encoding vertebrate activin receptor

PT polypeptides - useful as probes for detecting similar sequences and

PT for investigating the function of the receptor in conditions such as

PT carcinogenesis, wound healing and disorders of the immune, central

PT nervous and reproductive systems

XX Disclosure; Page -: 28pp; English.

XX This sequence represents a human activin receptor polypeptide. The

CC nucleic acid molecules of the invention are useful as probes for the

CC identification of additional members of the activin/TGF-superfamily of

CC receptor proteins, and the coding sequences can be used for the

CC recombinant expression of the receptor proteins or functional fragments

CC of them. They may also be used to study the function and activity of

CC activin receptor polypeptides in cells and to identify agents which will

CC modulate activin receptor expression and activity for use in treating

CC conditions such as carcinogenesis, wound healing, disorders of the

CC immune or central nervous systems and especially the reproductive system

CC (where they may be used to control fertility in humans, domestic and

CC commercial animals).

CC NOTE: This sequence does not appear in the specification but has been

CC created from the mouse activin receptor sequence (represented in

CC AAW93203) as described in the specification.

XX Sequence 513 AA;

SQ Query Match 100.0%; Score 2770; DB 20; Length 513;

Best Local Similarity 100.0%; Pred. No. 2.2e-271;

Matches 513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAALKAFVFLISCSGAILGRSETQCLFFNANWEKDRNTQGVPCYGDKRRHC 60

Db 1 MGAALKAFVFLISCSGAILGRSETQCLFFNANWEKDRNTQGVPCYGDKRRHC 60

QY 61 FATWKNISGSIIVKQGCWLLDDINCYDRDTCVCKKDSPEVYFCCCEGNCNEKFSYPPEM 120

Db 61 FATWKNISGSIIVKQGCWLLDDINCYDRDTCVCKKDSPEVYFCCCEGNCNEKFSYPPEM 120

QY 121 EVTQTSNPVTPKPPYYNLLYSVLPLMLIAGIVICAFWYVRHMKMAYPPVLVPTQDGP 180

Db 121 EVTQTSNPVTPKPPYYNLLYSVLPLMLIAGIVICAFWYVRHMKMAYPPVLVPTQDGP 180

QY 181 PPPSPLLGLKPLQLEVKARGFGVCWKQAQLLNEYVAVKIFPIQDKSQWNEYEYVSLPG 240

Db 181 PPPSPLLGLKPLQLEVKARGFGVCWKQAQLLNEYVAVKIFPIQDKSQWNEYEYVSLPG 240

QY 241 MKHENILOFIGAERKGTSDVDLMLITAFHEKGSLSDFLKANYVSWNOLCHIAETMARGL 300

Db 241 MKHENILOFIGAERKGTSDVDLMLITAFHEKGSLSDFLKANYVSWNOLCHIAETMARGL 300

QY 301 AYLHEDIPLGDKGHPATSHRDIKSNVLLKNNLTACIADFGLALKFPAKGSAGDTHGOV 360

Db 301 AYLHEDIPLGDKGHPATSHRDIKSNVLLKNNLTACIADFGLALKFPAKGSAGDTHGOV 360

QY 361 GTRRYMAPEVLGAINFORDAFRLIDMTYAMGLVLMELASRCTAADGPVDEYMLPFEERIG 420

Db 361 GTRRYMAPEVLGAINFORDAFRLIDMTYAMGLVLMELASRCTAADGPVDEYMLPFEERIG 420

QY 421 QHPSLEDQEVVHHKKRPVLDYQKHAGWAMLCETIEECWDHDAEALRSAGCVGERIT 480

Db 421 QHPSLEDQEVVHHKKRPVLDYQKHAGWAMLCETIEECWDHDAEALRSAGCVGERIT 480

QY 481 QMORLTNIITTEDIVTVTMVTNVDFPPKRESSL 513

Db 481 QMORLTNIITTEDIVTVTMVTNVDFPPKRESSL 513

RESULT 2

AAB47027

ID AAB47027 standard; Protein; 513 AA.

XX

AC AAB47027;

XX 29-MAR-2001 (first entry)

XX Human activin receptor.

DE Mouse; human; rat; Xenopus; activin receptor; ligand binding domain;

XX transmembrane domain; receptor domain; serine kinase; TGF-beta;

KW transforming growth factor-beta; carcinogenesis; cancer;

KW wound healing.

XX Homo sapiens.

OS

XX

FT Key Location/Qualifiers

FT Peptide 1..20

FT /note= "Secretion signal peptide"

XX US6162896-A.

XX 19-DEC-2000.

XX 07-JUN-1995; 95US-0476123.

XX 08-MAY-1992; 92US-0880220.

PR 10-MAY-1991; 91US-0698709.

PR 09-OCT-1991; 91US-0773229.

PR 02-SEP-1994; 94US-0300584.

XX (SALK ) SALK INST BIOLOGICAL STUDIES.

XX Tsuchida K, Vale WW, Mathews LW;

PI N-PSDB; AAC85299.

XX WPI; 2001-090408/10.

DR Novel vertebrate activin receptor having extracellular ligand binding

XX domain, transmembrane domain and intracellular serine/threonine kinase

PT domain, transmembrane domain and intracellular serine/threonine kinase

PT healing

XX Claim 11; Page -: 33pp; English.

XX This sequence shows a human-derived activin receptor. The activin

XX receptors of the invention comprise three distinct domains: an

XX extracellular, ligand binding domain, a hydrophobic, transmembrane

XX domain and an intracellular, receptor domain having serine kinase-like

XX activity. These proteins have binding affinity for at least one

XX member of the activin/TGF-beta superfamily of polypeptide growth

XX factors. The activin receptor proteins of the invention can be

XX employed for a variety of therapeutic uses, e.g. to block receptors.

XX The presence of the soluble proteins will compete with functional

XX ligand for the receptor, preventing the formation of a functional

XX receptor-ligand complex, thereby blocking the normal regulatory

XX action of the complex. The receptor proteins are useful for the

XX diagnosis and therapeutic management of carcinogenesis, wound healing,

XX disorders of the immune, reproductive, or central nervous systems.

XX Note: This sequence is not shown in the specification but is derived

XX from the mouse-derived activin receptor sequence (see AAB47025).

XX

SQ Sequence 513 AA;

Query Match 100.0%; Score 2770; DB 22; Length 513;

Best Local Similarity 100.0%; Pred. No. 2.2e-271;

Matches 513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAALKAFVFLISCSGAILGRSETQCLFFNANWEKDRNTQGVPCYGDKRRHC 60

Db 1 MGAALKAFVFLISCSGAILGRSETQCLFFNANWEKDRNTQGVPCYGDKRRHC 60

QY 61 FATWKNISGSIIVKQGCWLLDDINCYDRDTCVCKKDSPEVYFCCCEGNCNEKFSYPPEM 120

Db 61 FATWKNISGSIIVKQGCWLLDDINCYDRDTCVCKKDSPEVYFCCCEGNCNEKFSYPPEM 120

QY 121 EVTQTSNPVTPKPPYYNILLSLVPLMLIAGIVICAFWVYRHHKMAYPVPLVPTQDPGP 180  
Db 121 EVTQTSNPVTPKPPYYNILLSLVPLMLIAGIVICAFWVYRHHKMAYPVPLVPTQDPGP 180  
QY 181 PPPSPLGLKPLQLLEVKGARGFCVWKAQLLNEYVAVKIFPIQDKQSQWNEYEYVSLPG 240  
Db 181 PPPSPLGLKPLQLLEVKGARGFCVWKAQLLNEYVAVKIFPIQDKQSQWNEYEYVSLPG 240  
QY 241 MKHENILOFTGAERKGTSDVDLWLTAFHEKGSLSDFLKANVVSNNOLCHIAETMARGL 300  
Db 241 MKHENILOFTGAERKGTSDVDLWLTAFHEKGSLSDFLKANVVSNNOLCHIAETMARGL 300  
QY 301 AYLHEDIPLGDKGHPAISHRDIKSNVLLKNNLTACIADFGALKEAGKSAGDTHGOV 360  
Db 301 AYLHEDIPLGDKGHPAISHRDIKSNVLLKNNLTACIADFGALKEAGKSAGDTHGOV 360  
QY 361 GTRYMAPEVLEGAINFOADFLRIDMYAGLVLMELASRCTAAGDPVDEYMLPFEIEIG 420  
Db 361 GTRYMAPEVLEGAINFOADFLRIDMYAGLVLMELASRCTAAGDPVDEYMLPFEIEIG 420  
QY 421 QHPSLEDMDQEVVHHKKRPVLRDYWKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480  
Db 421 QHPSLEDMDQEVVHHKKRPVLRDYWKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480  
QY 481 QMORLTNIITTEDIVTVVTWTVNVDPPPKSSSL 513  
Db 481 QMORLTNIITTEDIVTVVTWTVNVDPPPKSSSL 513

RESULT 3  
AAO14127  
ID: AAO14127 standard; Protein: 513 AA.  
XX AAO14127;  
AC AAO14127;  
DT 07-MAY-2002 (first entry)  
XX Protein of a human-derived activin receptor.  
DE Activin receptor; cloning; recombinant; TGF-beta; ligand-binding;  
KW superfamily; trans-membrane; receptor domain; serine kinase; diagnosis;  
KW therapeutic management; carcinogenesis; wound healing; protein therapy;  
KW immune; reproductive; central nervous system; activin-dependent tumour;  
KW brain neuron; abortion; livestock; twinning; agonist; cytostatic;  
KW wound healing; transplant organ rejection; vulnery; immunosuppressive;  
KW transforming growth factor-beta; human.  
OS Homo sapiens.  
XX Key Location/Qualifiers  
FH Region 1..10  
FT /note= "Hydrophobic region"  
FT Region 119..142  
FT /note= "Membrane-spanning region"  
XX US2001039036-A1.  
XX 08-NOV-2001.  
XX 19-DEC-2000; 2000US-0742684.  
XX 07-JUN-1995; 95US-0476123.  
PR 08-MAY-1992; 92US-0880220.  
PR 10-MAY-1991; 91US-0698709.  
PR 09-OCT-1991; 91US-0773229.  
PR 02-SEP-1994; 94US-0300584.  
XX (SALK ) SALK INST BIOLOGICAL STUDIES.  
XX Mathews LS, Vale WW, Tsuchida K;  
XX WPI: 2002-040721/05.  
DR N-PSDB; AAK98725.

XX This sequence represents the protein of a human-derived activin receptor.  
PT The invention relates to cloning and recombinant production of  
PT receptor(s) of the activin/TGF-beta (transforming growth factor-beta)  
PT superfamily. The invention has identified and characterised members of a  
PT new superfamily of receptor proteins which comprise three distinct  
PT domains: an extracellular, ligand-binding domain, a hydrophobic, trans-  
PS membrane domain, and an intracellular, receptor domain having serine  
PS kinase-like activity. The receptor proteins and antibodies to these  
XX proteins are useful in the diagnosis and therapeutic management of  
CC carcinogenesis, wound healing, disorders of the immune, reproductive, or  
CC central nervous systems. The receptor proteins of the invention can be  
CC used in protein therapy. These may further be used to diagnose or treat  
CC activin-dependent tumours, enhance the survival of brain neurons, induce  
CC abortion in livestock and other domesticated animals, and induce twinning  
CC in livestock and other domesticated animals. The DNAs are useful as  
CC probes for identifying additional members of the superfamily of receptor  
CC proteins, and as coding sequences which can be used for the recombinant  
CC expression of the receptor proteins. Agonists for TGF-beta specific  
CC receptors can be used to stimulate wound healing, to suppress growth of  
CC TGF-beta sensitive tumours, or to suppress immune response (thus prevent  
CC rejection of transplant organ). The receptor proteins of the invention  
CC have cytostatic, vulnery, and immunosuppressive activity.  
CC NOTE: This sequence is not shown in the specification. It has been  
CC created from the sequence AAO14118 and information provided on page 12 of  
CC the specification.  
XX Sequence 513 AA;  
SQ Query Match 100.0%; Score 2770; DB 23; Length 513;  
Best Local Similarity 100.0%; Pred. No. 2.2e-271;  
Matches 513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGAALKAFVFLISCSGAILGRSETQECILFFNANNEKDRNTQGVGPCYGDKKRRHC 60  
Db 1 MGAALKAFVFLISCSGAILGRSETQECILFFNANNEKDRNTQGVGPCYGDKKRRHC 60  
QY 61 FATWKNISGSIEIVKQGCWLDINCIDRTDCVEKKDSPEVYFCCEGNCMEKSFYEP 120  
Db 61 FATWKNISGSIEIVKQGCWLDINCIDRTDCVEKKDSPEVYFCCEGNCMEKSFYEP 120  
QY 121 EVTQTSNPVTPKPPYYNILLSLVPLMLIAGIVICAFWVYRHHKMAYPVPLVPTQDPGP 180  
Db 121 EVTQTSNPVTPKPPYYNILLSLVPLMLIAGIVICAFWVYRHHKMAYPVPLVPTQDPGP 180  
QY 181 PPPSPLGLKPLQLLEVKGARGFCVWKAQLLNEYVAVKIFPIQDKQSQWNEYEYVSLPG 240  
Db 181 PPPSPLGLKPLQLLEVKGARGFCVWKAQLLNEYVAVKIFPIQDKQSQWNEYEYVSLPG 240  
QY 241 MKHENILOFTGAERKGTSDVDLWLTAFHEKGSLSDFLKANVVSNNOLCHIAETMARGL 300  
Db 241 MKHENILOFTGAERKGTSDVDLWLTAFHEKGSLSDFLKANVVSNNOLCHIAETMARGL 300  
QY 301 AYLHEDIPLGDKGHPAISHRDIKSNVLLKNNLTACIADFGALKEAGKSAGDTHGOV 360  
Db 301 AYLHEDIPLGDKGHPAISHRDIKSNVLLKNNLTACIADFGALKEAGKSAGDTHGOV 360  
QY 361 GTRYMAPEVLEGAINFOADFLRIDMYAGLVLMELASRCTAAGDPVDEYMLPFEIEIG 420  
Db 361 GTRYMAPEVLEGAINFOADFLRIDMYAGLVLMELASRCTAAGDPVDEYMLPFEIEIG 420  
QY 421 QHPSLEDMDQEVVHHKKRPVLRDYWKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480  
Db 421 QHPSLEDMDQEVVHHKKRPVLRDYWKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480  
QY 481 QMORLTNIITTEDIVTVVTWTVNVDPPPKSSSL 513



XX Claim 29; Column 25-28; 28pp; English.

XX This sequence represents a mouse activin receptor polypeptide. The

XX nucleic acid molecules of the invention are useful as probes for the

XX identification of additional members of the activin/TGF-superfamily of

XX receptor proteins, and the coding sequences can be used for the

XX recombinant expression of the receptor proteins or functional fragments

XX of them. They may also be used to study the function and activity of

XX activin receptor polypeptides in cells and to identify agents which will

XX modulate activin receptor expression and activity for use in treating

XX conditions such as carcinogenesis, wound healing, disorders of the immune

XX or central nervous systems and especially the reproductive system (where

XX they may be used to control fertility in humans, domestic and commercial

XX animals).

XX Sequence 513 AA;

XX

XX Query Match 99.7%; Score 2763; DB 20; Length 513;

XX Best Local Similarity 99.4%; Pred. No. 1.1e-270;

XX Matches 510; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAALAFVAVFLISCSGAILGRSETQECLEFFNANWEKDRNTQGTGVCYGDGDKRRHC 60

DB 1 MGAALAFVAVFLISCSGAILGRSETQECLEFFNANWEKDRNTQGTGVCYGDGDKRRHC 60

QY 61 FATWKNISGIEIVKQGCWLDLINCVDCTCEKDSPEVYFCCGEGNMCNEKESYFPEM 120

DB 61 FATWKNISGIEIVKQGCWLDLINCVDCTCEKDSPEVYFCCGEGNMCNEKESYFPEM 120

QY 121 EVTQPTSNVTPKPPYNNILYSLVPLMLTAGIVICAFWYRHHKWAYPPVLVPTQDGP 180

DB 121 EVTQPTSNVTPKPPYNNILYSLVPLMLTAGIVICAFWYRHHKWAYPPVLVPTQDGP 180

QY 181 PPPSLLGLKPLQLLEVKARGFGCVKWAQLLNEYVAVKIFPIQDKQSWQNEYEYSLPG 240

DB 181 PPPSLLGLKPLQLLEVKARGFGCVKWAQLLNEYVAVKIFPIQDKQSWQNEYEYSLPG 240

QY 241 MKHENILQIFGAEKRGTSVDVLDLITAFHEKGSLSDFLKANYVSNWNLCHIAETMARGL 300

DB 241 MKHENILQIFGAEKRGTSVDVLDLITAFHEKGSLSDFLKANYVSNWNLCHIAETMARGL 300

QY 301 AYLHEDIPGLKDGHPAISHRDIKSNVLLKNLTACTADFLCALKFEAGKSAGDTHGOV 360

DB 301 AYLHEDIPGLKDGHPAISHRDIKSNVLLKNLTACTADFLCALKFEAGKSAGDTHGOV 360

QY 361 GTRRYMAPEVLGAINFORDAFLRDMYAMGLVWELASRCTAADGPVDEYMLFEEBIG 420

DB 361 GTRRYMAPEVLGAINFORDAFLRDMYAMGLVWELASRCTAADGPVDEYMLFEEBIG 420

QY 421 QHPSLEDQEVVVKKKRPVLRDYWKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480

DB 421 QHPSLEDQEVVVKKKRPVLRDYWKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480

QY 481 QMORLNTIITIEDIVVTVMNTVNDVFPKESL 513

DB 481 QMORLNTIITIEDIVVTVMNTVNDVFPKESL 513

RESULT 6

AAB14797

ID AAB14797 standard; Protein; 513 AA.

XX

XX AAB14797;

XX

XX 11-DEC-2000 (first entry)

XX

XX Mouse activin receptor.

XX

XX TGF-beta superfamily protein receptor; activin receptor; mouse; MR-1;

XX Drosophila morphogen receptor; morphogen analogue identification;

XX OP-1; BMP-2; bone morphogenetic protein-2; in vivo binding; antagonist;

XX agonist; osteosarcoma; Paget's disease; tissue regeneration;

XX tissue repair; insecticide.

XX Mus sp.

XX US6093547-A.

XX 25-JUL-2000.

XX 02-JUN-1995; 95US-0459951.

XX 16-DEC-1994; 94US-0357533.

XX 07-JUN-1993; 93US-0073199.

XX (CREA-) CREATIVE BIOMOLECULES INC.

XX Kuberampath T, Smart JE, Jin DF, Oppermann H.

XX WPI; 2000-531476/48.

XX Identifying morphogen analogs useful for designing morphogen agonists

XX and antagonists for therapeutic or diagnostic uses, comprises exposing

XX a candidate morphogen analog to a morphogen receptor-1.

XX Example 1; Column 43-48; 31pp; English.

XX The invention relates to a method of identifying a morphogen analogue

XX and predicting whether it is capable of in vivo binding to a morphogen

XX receptor. The method comprises determining whether the candidate

XX morphogen analogue binds to the Drosophila morphogen receptor MR-1

XX (AAB14794), its allelic and species variants, or its isolated ligand

XX binding domain. The method is useful for identifying morphogen

XX analogues which may be used in therapeutic, diagnostic and

XX experimental research applications as morphogen agonists or

XX antagonists. Morphogen antagonists may be used to modulate uncontrolled

XX differentiated tissue growth such as malignant transformations in

XX osteosarcoma or Paget's disease, and as insecticides, which can

XX interfere with insect growth and tissue development. Morphogen agonists

XX are used where tissue morphogenesis is desired, e.g., in the

XX regeneration of damaged tissue resulting from mechanical or chemical

XX trauma, degenerative diseases, or tissue destruction. Sequences

XX AAB14795-B14798 represent receptors for TGF-beta superfamily proteins

XX which were used to design degenerate PCR primers (AAA72309-A72312). In an

XX exemplification of the invention, the primers were used to isolate a

XX probe (AAA72308) from Drosophila genomic DNA which was in turn used to

XX isolate cDNA encoding Drosophila MR-1 (AAA72307). The present sequence

XX represents a mouse activin receptor.

XX

XX Sequence 513 AA;

XX

XX Query Match 99.7%; Score 2763; DB 21; Length 513;

XX Best Local Similarity 99.4%; Pred. No. 1.1e-270;

XX Matches 510; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAALAFVAVFLISCSGAILGRSETQECLEFFNANWEKDRNTQGTGVCYGDGDKRRHC 60

DB 1 MGAALAFVAVFLISCSGAILGRSETQECLEFFNANWEKDRNTQGTGVCYGDGDKRRHC 60

QY 61 FATWKNISGIEIVKQGCWLDLINCVDCTCEKDSPEVYFCCGEGNMCNEKESYFPEM 120

DB 61 FATWKNISGIEIVKQGCWLDLINCVDCTCEKDSPEVYFCCGEGNMCNEKESYFPEM 120

QY 121 EVTQPTSNVTPKPPYNNILYSLVPLMLTAGIVICAFWYRHHKWAYPPVLVPTQDGP 180

DB 121 EVTQPTSNVTPKPPYNNILYSLVPLMLTAGIVICAFWYRHHKWAYPPVLVPTQDGP 180

QY 181 PPPSLLGLKPLQLLEVKARGFGCVKWAQLLNEYVAVKIFPIQDKQSWQNEYEYSLPG 240

DB 181 PPPSLLGLKPLQLLEVKARGFGCVKWAQLLNEYVAVKIFPIQDKQSWQNEYEYSLPG 240

QY 241 MKHENILQIFGAEKRGTSVDVLDLITAFHEKGSLSDFLKANYVSNWNLCHIAETMARGL 300

DB 241 MKHENILQIFGAEKRGTSVDVLDLITAFHEKGSLSDFLKANYVSNWNLCHIAETMARGL 300

Qy 301 AYLEDIPGLKDGHPKPAISHRDIKSKVLLKNNLTACIADFGALALFEAGKSAGDTHGQV 360  
 Db 301 AYLEDIPGLKDGHPKPAISHRDIKSKVLLKNNLTACIADFGALALFEAGKSAGDTHGQV 360  
 Qy 361 GTRYMAPEVLEGAINFQDAFLRIDMYAMGLVWLWELASRCTAADGVPDEYMLPFEEIG 420  
 Db 361 GTRYMAPEVLEGAINFQDAFLRIDMYAMGLVWLWELASRCTAADGVPDEYMLPFEEIG 420  
 Qy 421 QHPSLEDQMEVVVHKKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEALRSAGCVGERIT 480  
 Db 421 QHPSLEDQMEVVVHKKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEALRSAGCVGERIT 480  
 Qy 481 QMQLTNIITTEDIVVTWMTNVDFFPKESSL 513  
 Db 481 QMQLTNIITTEDIVVTWMTNVDFFPKESSL 513

RESULT 7  
 AAB47025  
 ID AAB47025 standard; Protein: 513 AA.  
 XX  
 AC AAB47025;

29-MAR-2001 (first entry)  
 Mouse activin receptor.  
 DE Mouse; human; rat; Xenopus; activin receptor; ligand binding domain;  
 KW transmembrane domain; receptor domain; serine kinase; TGF-beta;  
 KW transforming growth factor-beta; carcinogenesis; cancer;  
 KW wound healing.  
 XX Mus musculus.

Key Location/Qualifiers  
 Peptide 1..19 /note= "Secretion signal peptide"  
 XX  
 XX US6162896-A.  
 PD 19-DEC-2000.  
 XX  
 PF 07-JUN-1995; 95US-0476123.  
 XX  
 PR 08-MAY-1992; 92US-0880220.  
 PR 10-MAY-1991; 91US-0698709.  
 PR 09-OCT-1991; 91US-0773229.  
 PR 02-SEP-1994; 94US-0300584.  
 XX  
 PA (SALK ) SALK INST BIOLOGICAL STUDIES.  
 XX  
 TS Tsuchida K, Vale WW, Mathews LW;  
 WPI: 2001-090408/10.  
 DR N-PSDB; AAC85297.

Novel vertebrate activin receptor having extracellular ligand binding domain, transmembrane domain and intracellular serine/threonine kinase domain is useful for diagnosing and treating e.g. carcinogenesis, wound healing  
 Claim 11; Column 27-30; 33pp; English.  
 This sequence shows a mouse-derived activin receptor. The activin receptors of the invention comprise three distinct domains: an extracellular, ligand binding domain, a hydrophobic, transmembrane domain and an intracellular, receptor domain having serine kinase-like activity. These proteins have binding affinity for at least one member of the activin/TGF-beta superfamily of polypeptide growth factors. The activin receptor proteins of the invention can be employed for a variety of therapeutic uses, e.g. to block receptors. The presence of the soluble proteins will compete with functional ligand for the receptor, preventing the formation of a functional

CC receptor-ligand complex, thereby blocking the normal regulatory action of the complex. The receptor proteins are useful for the diagnosis and therapeutic management of carcinogenesis, wound healing, disorders of the immune, reproductive, or central nervous systems.  
 XX  
 SQ Sequence 513 AA;  
 Query Match 99.7%; Score 2763; DB 22; Length 513;  
 Best Local Similarity 99.4%; Pred. NO. 1.1e-270;  
 Matches 510; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MGAATAKLAFAVFLISCSGAILGRSETQCLFFNANWEKDRNTQGTGVEPCYGDKKRRHC 60  
 Db 1 MGAATAKLAFAVFLISCSGAILGRSETQCLFFNANWEKDRNTQGTGVEPCYGDKKRRHC 60  
 Qy 61 FATWKNISGIEIVKQGCWLDIDNCYDRDTCVEKKDSEVYFCCCEGNNCKEFSYFPEM 120  
 Db 61 FATWKNISGIEIVKQGCWLDIDNCYDRDTCIEKKDSEVYFCCCEGNNCKEFSYFPEM 120  
 Qy 121 EVTQPTSNPVTPKPPYYNLLYSLVPLMLIAGIVICAFWVYRHHKMAPVLPVPTQDFGP 180  
 Db 121 EVTQPTSNPVTPKPPYYNLLYSLVPLMLIAGIVICAFWVYRHHKMAPVLPVPTQDFGP 180  
 Qy 181 PPSPLLLGLKPLQLLEVKGARGGCVWKAQLLNEYVAVKIFPIQDKQSMONEYEYVSLPG 240  
 Db 181 PPSPLLLGLKPLQLLEVKGARGGCVWKAQLLNEYVAVKIFPIQDKQSMONEYEYVSLPG 240  
 Qy 241 MKHENILQFIGAEKRGTSVDVLDLITAFHEKGSLSDFLKANVSWNQLCHIAETMARGL 300  
 Db 241 MKHENILQFIGAEKRGTSVDVLDLITAFHEKGSLSDFLKANVSWNQLCHIAETMARGL 300  
 Qy 301 AYLEDIPGLKDGHPKPAISHRDIKSKVLLKNNLTACIADFGALALFEAGKSAGDTHGQV 360  
 Db 301 AYLEDIPGLKDGHPKPAISHRDIKSKVLLKNNLTACIADFGALALFEAGKSAGDTHGQV 360  
 Qy 361 GTRYMAPEVLEGAINFQDAFLRIDMYAMGLVWLWELASRCTAADGVPDEYMLPFEEIG 420  
 Db 361 GTRYMAPEVLEGAINFQDAFLRIDMYAMGLVWLWELASRCTAADGVPDEYMLPFEEIG 420  
 Qy 421 QHPSLEDQMEVVVHKKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEALRSAGCVGERIT 480  
 Db 421 QHPSLEDQMEVVVHKKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEALRSAGCVGERIT 480  
 Qy 481 QMQLTNIITTEDIVVTWMTNVDFFPKESSL 513  
 Db 481 QMQLTNIITTEDIVVTWMTNVDFFPKESSL 513

RESULT 8  
 AAO14118  
 ID AAO14118 standard; Protein: 513 AA.  
 XX  
 AC AAO14118;  
 XX  
 DT 07-MAY-2002 (first entry)  
 XX  
 DE Protein of a mouse-derived activin receptor.  
 XX  
 KW Mouse; activin receptor; cloning; recombinant; TGF-beta; ligand-binding; superfamily; trans-membrane; receptor domain; serine kinase; diagnosis; therapeutic management; carcinogenesis; wound healing; protein therapy; immune; reproductive; central nervous system; activin-dependent tumour; brain neuron; abortion; livestock; twinning; probe; agonist; cytostatic; wound healing; transplant organ rejection; vulnerability; immunosuppressive; transforming growth factor-beta.  
 XX Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..10  
 FT Region /note= "Hydrophobic region"  
 FT Region 119..142  
 FT Region /note= "Membrane-spanning region"

XX PN US2001039036-A1.  
XX PD 08-NOV-2001.  
XX PF 19-DEC-2000; 2000US-0742684.  
XX PR 07-JUN-1995; 95US-0476123.  
XX PR 08-MAY-1992; 92US-0880220.  
XX PR 10-MAY-1991; 91US-0698709.  
XX PR 09-OCT-1991; 91US-0773229.  
XX PR 02-SEP-1994; 94US-0300384.  
XX (SALK ) SALK INST BIOLOGICAL STUDIES.  
XX PA Mathews LS, Vale WW, Tsuchida K;  
XX PI WPI; 2002-040721/05.  
XX PS N-PSDB; AAK98720.  
XX  
XX New receptor proteins having an extracellular ligand-binding domain, a hydrophobic trans-membrane domain, and an intracellular receptor domain, useful for diagnosing or treating carcinogenesis, wound healing or immune disorders  
XX  
XX Claim 5; Page 15-16; 33pp; English.  
XX  
XX This sequence represents the protein of a mouse-derived activin receptor. The invention relates to cloning and recombinant production of receptor(s) of the activin/TGF-beta (transforming growth factor-beta) superfamily. The invention has identified and characterised members of a new superfamily of receptor proteins which comprise three distinct domains: an extracellular, ligand-binding domain, a hydrophobic, trans-membrane domain, and an intracellular, receptor domain having serine kinase-like activity. The receptor proteins and antibodies to these proteins are useful in the diagnosis and therapeutic management of carcinogenesis, wound healing, disorders of the immune, reproductive, or central nervous systems. The receptor proteins of the invention can be used in protein therapy. These may further be used to diagnose or treat activin-dependent tumours, enhance the survival of brain neurons, induce abortion in livestock and other domesticated animals, and induce twinning in livestock and other domesticated animals. The DNAs are useful as probes for identifying additional members of the superfamily of receptor proteins, and as coding sequences which can be used for the recombinant expression of the receptor proteins. Agonists for TGF-beta specific receptors can be used to stimulate wound healing, to suppress growth of TGF-beta sensitive tumours, or to suppress immune response (thus prevent rejection of transplant organ). The receptor proteins of the invention have cytostatic, vulnerary, and immunosuppressive activity.  
XX  
XX Sequence 513 AA;  
SQ  
Query Match 99.7%; Score 2763; DB 23; Length 513;  
Best Local Similarity 99.4%; Pred. No. 1,1e-270;  
Matches 510; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGAALKAFVFLISGSGAILGRSTQCLFFNANWEKDRNTQTVGPEYGDGDKRRHC 60  
DB 1 MGAALKAFVFLISGSGAILGRSTQCLFFNANWEKDRNTQTVGPEYGDGDKRRHC 60  
QY 61 FATWKNISGSIETVKGWGLDDINCVDCTDCEKDSPEVYFCCCEGNCNEKFSYFFPEM 120  
DB 61 FATWKNISGSIETVKGWGLDDINCVDCTDCEKDSPEVYFCCCEGNCNEKFSYFFPEM 120  
QY 121 EVTQPTSNVTPKPPYNNILYSLVPLMLIAGIVICAFWYRHHKMAYPVLPVTPQDGP 180  
DB 121 EVTQPTSNVTPKPPYNNILYSLVPLMLIAGIVICAFWYRHHKMAYPVLPVTPQDGP 180  
QY 181 PPPSPLLGLKPLQLLEVARGFGCWKAQLLNEYVAVKFIPTQDKSQWNEYEYVSLPG 240  
DB 181 PPPSPLLGLKPLQLLEVARGFGCWKAQLLNEYVAVKFIPTQDKSQWNEYEYVSLPG 240  
QY 241 MKHENILQFIGAEKRGTSVDVLDLITAFHEKGSLSDFLKANVSWNELCHIAETMARGL 300

Db 241 MKHENILQFIGAEKRGTSVDVLDLITAFHEKGSLSDFLKANVSWNELCHIAETMARGL 300  
QY 301 AYLEDIPGLKDGHPKPAISHRDIKSKNVLNNLTACIADFGALKFAGKSAGDTHGOV 360  
Db 301 AYLEDIPGLKDGHPKPAISHRDIKSKNVLNNLTACIADFGALKFAGKSAGDTHGOV 360  
QY 361 GTRRYMAPEVLEGAINFORDAFRLIDMYAMGLVWLWELASRCAADGPVDEYMLPFEIEIG 420  
Db 361 GTRRYMAPEVLEGAINFORDAFRLIDMYAMGLVWLWELASRCAADGPVDEYMLPFEIEIG 420  
QY 421 QHPSLEDQEVVVVHKRPVLRDYWKHAGMAMLCETIEECWHDHDAEARLSAGCVGERIT 480  
Db 421 QHPSLEDQEVVVVHKRPVLRDYWKHAGMAMLCETIEECWHDHDAEARLSAGCVGERIT 480  
QY 481 QMRLTNIITTEDIVTVVMTVNTVDFPPESSSL 513  
Db 481 QMRLTNIITTEDIVTVVMTVNTVDFPPESSSL 513  
RESULT 9  
AAR29581  
ID AAR29581 standard; Protein; 513 AA.  
XX  
XX AC AAR29581;  
XX  
XX 19-APR-1993 (first entry)  
XX Mouse activin receptor.  
XX  
XX Activin receptor; mouse; Xenopus; human; extracellular; ligand binding; hydrophobic; trans-membrane; intracellular; receptor; domain; serine kinase-like; activity; probe; superfamily; secretion signal; golgi membrane; diagnosis; treatment; activin-dependent tumour; brain; neuron; abortion; twinning; wound healing; TGF-beta; immune response; liver regeneration.  
XX  
XX Mus musculus.  
XX  
XX WO9220793-A.  
XX 26-NOV-1992.  
XX  
XX 08-MAY-1992; 92WO-US03825.  
XX  
XX 10-MAY-1991; 91US-0698709.  
XX 09-OCT-1991; 91US-0773229.  
XX (SALK ) SALK INST BIOLOGICAL STUDIES.  
XX  
XX Mathews LS, Vale WW;  
XX  
XX WPI; 1992-415771/50.  
XX N-PSDB; AAK31910.  
XX  
XX New member of activin-transforming growth factor beta super-family - for diagnosis and treatment of cancer and disorders of the immune, reproductive or central nervous system  
XX  
XX Disclosure; Page 42-45; 68pp; English.  
XX  
XX The sequences given in AAR29581-83 represent activin receptors from mouse, Xenopus and human respectively. Each of these proteins comprise three distinct domains: an extracellular, ligand binding domain, a hydrophobic, trans-membrane domain and an intracellular, receptor domain having serine kinase-like activity. The DNA sequences encoding these proteins can be used as probes for the identification of additional members of this superfamily of receptor molecules. The proteins may further comprise a second hydrophobic domain at the amino terminal which comprises a secretion signal sequence which promotes the intracellular transport of the initially expressed receptor protein across the golgi membrane. These receptor proteins can be used to develop agents for the diagnosis and/or treatment of eg.

CC activin-dependent tumours, for enhancing the survival of brain  
CC neurons, for inducing abortion or twinning in livestock, for  
CC stimulating wound healing, for suppression of growth of TGF-beta  
CC sensitive tumours, for suppressing immune response, for promoting  
CC liver regeneration and for stimulating some immune responses.

XX Sequence 513 AA;

Query Match 99.6%; Score 2758; DB 13; Length 513;  
Best Local Similarity 99.2%; Pred. No. 3.6e-270;  
Matches 509; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGAALAFVFLISCSGAILGRSETQECLEFFNANWEKDRDTNOTGVPCYGDKRRHC 60  
Db 1 MGAALAFVFLISCSGAILGRSETQECLEFFNANWEKDRDTNOTGVPCYGDKRRHC 60  
Qy 61 FATWKNISGSIEIVKQGCWLDINDCYDTCIEKDSPEVYFCCCEGNMCKNEKFSYFPEM 120  
Db 61 FATWKNISGSIEIVKQGCWLDINDCYDTCIEKDSPEVYFCCCEGNMCKNEKFSYFPEM 120  
Qy 121 EVTQPTSNPVTPKPPYNNILLYSLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDGP 180  
Db 121 EVTQPTSNPVTPKPPYNNILLYSLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDGP 180  
Qy 181 PPPSLGLKPLQLLEVKARGFCVWKAQLLNEYVAVKIPPTQDKOSWONEVEYVSLPG 240  
Db 181 PPPSLGLKPLQLLEVKARGFCVWKAQLLNEYVAVKIPPTQDKOSWONEVEYVSLPG 240  
Qy 241 MKHENILOFICAEKRGTSVDVLDLITAFHEKGSLSDFLKNVYVSNOLCHIAETMARGL 300  
Db 241 MKHENILOFICAEKRGTSVDVLDLITAFHEKGSLSDFLKNVYVSNOLCHIAETMARGL 300  
Qy 301 AYLEDIPGLKDGHPKPAISHRDIKSKNVLKNNLTACIADFGALKEACKSAGDTHGQV 360  
Db 301 AYLEDIPGLKDGHPKPAISHRDIKSKNVLKNNLTACIADFGALKEACKSAGDTHGQV 360  
Qy 361 GTRRYMAPEVLEGAINFORDAFLRIDMYAGLVWLWELASRCTAADGVPDEYMLPFEEIG 420  
Db 361 GTRRYMAPEVLEGAINFORDAFLRIDMYAGLVWLWELASRCTAADGVPDEYMLPFEEIG 420  
Qy 421 QHPSLEDQEVVYVHKRPVLDYVQKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480  
Db 421 QHPSLEDQEVVYVHKRPVLDYVQKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480  
Qy 481 QMORLTNIITTEDIVVTWVTNVDFFPKESSL 513  
Db 481 QMORLTNIITTEDIVVTWVTNVDFFPKESSL 513

RESULT 10  
AAW26359  
AAW26359 standard; Protein; 521 AA.

AC AAW26359;  
XX 02-DEC-1997 (first entry)  
XX Mouse activin receptor.

DE Activin receptor; neuronal cell-specific receptor; mouse;  
KW neurodegenerative disease; diagnosis.  
KW Mus musculus.

OS Key Location/Qualifiers

FT Misc-difference 1 /note= "residue 1 is (optionally protected) Met  
FT /note= "or is replaced by hydrogen"

FT Peptide /note= "characteristic peptide of activin receptor  
FT (Claim 1)"

PN EP771873-A2.

XX 07-MAY-1997.  
XX 25-OCT-1996; 96EP-0117125.  
XX 04-JUL-1996; 96JP-0174909.  
XX 27-OCT-1995; 95JP-0280939.  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX Nakamura T, Shouji H, Sugino H;  
XX WPI; 1997-247415/23.  
XX N-PSDB; AAT84517.  
XX Neuronal activin receptor protein and DNA - for use in drug  
XX screening assays and diagnosis of neurodegenerative diseases  
XX Claim 4; Page 30-31; 40pp; English.  
XX This polypeptide sequence comprises a novel mouse activin receptor  
XX whose expression is specific to the neuronal system and the whole  
XX embryo. The sequence was deduced from a cDNA clone (AAT84517)  
XX isolated from a mouse embryonal carcinoma cell line p19 whose  
XX neuronal differentiation had been induced by retinoic acid. The  
XX sequence includes an octapeptide (see AAW26360) that is highly  
XX conserved in activin receptors, also being found in human and frog  
XX sequences. The receptor, and DNA encoding it, can be used for  
XX ligand determination, preparation of antibodies, construction of  
XX recombinant receptor protein expression systems, development of  
XX receptor binding assays and screening for pharmaceutical candidates,  
XX drug design based on structurally similar ligand receptors,  
XX construction of probes and primers (see AAT84518-19) for gene  
XX detection (useful for the diagnosis of neurodegenerative diseases),  
XX and for gene therapy.

XX Sequence 521 AA;

Query Match 99.1%; Score 2744; DB 18; Length 521;  
Best Local Similarity 97.9%; Pred. No. 9.7e-269;  
Matches 509; Conservative 3; Mismatches 0; Indels 8; Gaps 1;

Qy 2 GAAALAFVFLISCSGAILGRSETQECLEFFNANWEKDRDTNOTGVPCYGDKRRHCF 61  
Db 2 GAAALAFVFLISCSGAILGRSETQECLEFFNANWEKDRDTNOTGVPCYGDKRRHCF 61  
Qy 62 ATWKNISGSIEIVKQGCWLDINDCYDTCIEKDSPEVYFCCCEGNMCKNEKFSYFPEME 121  
Db 62 ATWKNISGSIEIVKQGCWLDINDCYDTCIEKDSPEVYFCCCEGNMCKNEKFSYFPEME 121  
Qy 122 VTQPTSNPVTPKPPYNNILLYSLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQ---- 176  
Db 122 VTQPTSNPVTPKPPYNNILLYSLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQAFHI 181  
Qy 177 ---DPGPPPPPLGLKPLQLLEVKARGFCVWKAQLLNEYVAVKIPPTQDKOSWONEY 233  
Db 182 MIEDPGPPPPPLGLKPLQLLEVKARGFCVWKAQLLNEYVAVKIPPTQDKOSWONEY 241  
Qy 234 EYVSLPMKHNILQFICAEKRGTSVDVLDLITAFHEKGSLSDFLKNVYVSNOLCHIA 293  
Db 242 EYVSLPMKHNILQFICAEKRGTSVDVLDLITAFHEKGSLSDFLKNVYVSNOLCHIA 301  
Qy 294 ETWARGLAYLHEDIPGLKDGHPKPAISHRDIKSKNVLKNNLTACIADFGALKEACKS 353  
Db 302 ETWARGLAYLHEDIPGLKDGHPKPAISHRDIKSKNVLKNNLTACIADFGALKEACKS 361  
Qy 354 GDTHGQVGTFRYMAPEVLEGAINFORDAFLRIDMYAGLVWLWELASRCTAADGVPDEYML 413  
Db 362 GDTHGQVGTFRYMAPEVLEGAINFORDAFLRIDMYAGLVWLWELASRCTAADGVPDEYML 421  
Qy 414 PFEEIGQHPSLQEDQEVVYVHKRPVLDYVQKHAGMAMLCETIEECWDHDAEARLSAG 473  
Db 422 PFEEIGQHPSLQEDQEVVYVHKRPVLDYVQKHAGMAMLCETIEECWDHDAEARLSAG 481



QY 474 CVGERITOMORLTNIITTDIVVTWTVNVDPPKESL 513  
 DB 482 CVGERITOMORLTNIITTDIVVTWTVNVDPPKESL 521

## RESULT 11

AAW93204  
 ID AAW93204 standard; Protein; 510 AA.

AC AAW93204;

XX 27-MAY-1999 (first entry)

DE Xenopus activin receptor protein.

XX Activin receptor; activin/TGF-superfamily; receptor protein; function;  
 XX activity; modulate; treatment; carcinogenesis; wound healing; fertility;  
 XX immune system disorder; central nervous system disorder;  
 KW reproductive system.

XX Xenopus sp.

XX US885794-A.

XX 23-MAR-1999.

XX 02-SEP-1994; 94US-0300584.

XX 08-MAY-1992; 92US-0880220.

XX 10-MAY-1991; 91US-0698709.

XX 09-OCT-1991; 91US-0773229.

XX 02-SEP-1994; 94US-0300584.

PA (SALK ) SALK INST BIOLOGICAL STUDIES.

XX Mathews LS, Vale WW;

XX WPI; 1999-228534/19.

XX N-PSDB; AAX22684.

Isolated nucleic acid molecules encoding vertebrate activin receptor polypeptides - useful as probes for detecting similar sequences and for investigating the function of the receptor in conditions such as carcinogenesis, wound healing and disorders of the immune, central nervous and reproductive systems

XX Claim 29; Column 33-36; 28pp; English.

XX This sequence represents a Xenopus sp. activin receptor polypeptide. The nucleic acid molecules of the invention are useful as probes for the identification of additional members of the activin/TGF-superfamily of receptor proteins, and the coding sequences can be used for the recombinant expression of the receptor proteins or functional fragments of them. They may also be used to study the function and activity of activin receptor polypeptides in cells and to identify agents which will modulate activin receptor expression and activity for use in treating conditions such as carcinogenesis, wound healing, disorders of the immune or central nervous systems and especially the reproductive system (where they may be used to control fertility in humans, domestic and commercial animals).

XX Sequence 510 AA;

Query Match 71.2%; Score 1971.5; DB 20; Length 510;  
 Best Local Similarity 67.9%; Pred. No. 1.7e-190;  
 Matches 349; Conservative 85; Mismatches 75; Indels 5; Gaps 3;

QY 1 MGAANKAFAYFLISCSGAILGRSETOECLFFNANNEKORTNOTGVPCYGDKRRHC 60

DB 1 MGASVALTFLLLATFRAGSGHDEYETRECIYYNANNELEKTNOSGESGEGRKRLHC 60

QY 61 FATWKNISGSIEIVKQGCWLDIDNCYDRTDCVEKKDSPEVYFCCCGMNCNKFVSFPEM 120

DB 61 YASWRNNSGFIELVKKGCWLDIDNCYDROBCTIAKENPQVFCCCBGNTCNKFTLPEV 120  
 QY 121 EVTQPTSNPTKPPYYNILLYSILVPLMLTAGIVICAFWYRHHKWAYPPVLVPTQDGP 180  
 DB 121 ETDFPKQ---PSASVLNLIYISLLPIVGLSMALLAFWYRHHKPPYGHVEI-NEDFGL 176  
 QY 181 PPSPLGLKPLQLLEVKARGCGVWKAKQLLNEYVAVKIFPIQDKSQSWONEYVSLPG 240  
 DB 177 PPSPLVGLKPLQLLEIKARGCGVWKARLLNEYVAVKIFPVODKQSQWCEKEIFTPG 236  
 QY 241 MKHENILOFTCAEKRGTSVDVLDLWLTAFHEKGSLSDELKANVYSNOLCHIAETMARGL 300  
 DB 237 MKHENLEFIAAEKRGSNLEMLWLTAFHDKGSLDYILKGNLVSNELCHITETMARGL 296  
 QY 301 AYLEDIPGLK-DGHRKPAISHRDIKSKNVLKNNLTACIADFGALKFAGKSAGDTHGQ 359  
 DB 297 AYLEDVPRCKGEGHKPAIAHRDFKSKNVLRLNDLTAILADFGAVRFPKPGDTHGQ 356  
 QY 360 VGTTRYMAPEVLEGAINFQDAFLRDMYAMGLVILVELASRCTAADGPVDEYMLPEEEI 419  
 DB 357 VGTTRYMAPEVLEGAINFQDSFLRDMYAMGLVILWEIVSRCTAADGPVDEYMLPEEEI 416  
 QY 420 GQHPSLQEDMQEVVYVHKRPPVLDYVQKHAGMAMLCETIEECWDHDAEARLSAGCVGERI 479  
 DB 417 GQHPSLQEDLQEVVYVHKRPPVLDYVQKHAGMAMLCETIEECWDHDAEARLSAGCVGERI 476  
 QY 480 TOMORLTNIITTDIVVTWTVNVDPPKESL 513  
 DB 477 SQIRKSVNGTSDCLVSVITSVTNVDLPPKESI 510

## RESULT 12

AAW47026  
 ID AAW47026 standard; Protein; 510 AA.

XX AAW47026;

XX 29-MAR-2001 (first entry)

DE Xenopus activin receptor.

XX Mouse; human; rat; Xenopus; activin receptor; ligand binding domain;  
 KW transmembrane domain; receptor domain; serine kinase; TGF-beta;  
 KW transforming growth factor-beta; carcinogenesis; cancer;  
 KW wound healing.

XX Xenopus laevis.

XX Key Location/Qualifiers  
 FT Peptide 1..20  
 FT /note= "Secretion signal peptide"

XX US6162896-A.

XX 19-DEC-2000.

XX 07-JUN-1995; 95US-0476123.

XX 08-MAY-1992; 92US-0880220.

XX 10-MAY-1991; 91US-0698709.

XX 09-OCT-1991; 91US-0773229.

XX 02-SEP-1994; 94US-0300584.

XX (SALK ) SALK INST BIOLOGICAL STUDIES.

XX Tsuchida K, Vale WW, Mathews LW;

XX WPI; 2001-090408/10.

XX N-PSDB; AAC85298.

Novel vertebrate activin receptor having extracellular ligand binding domain, transmembrane domain and intracellular serine/threonine kinase

PT domain is useful for diagnosing and treating e.g. carcinogenesis, wound  
 PT healing

PS Claim 11; Column 33-36; 33pp; English.

XX This sequence shows a frog-derived activin receptor. The activin  
 CC receptors of the invention comprise three distinct domains: an  
 CC extracellular, ligand binding domain, a hydrophobic, transmembrane  
 CC domain and an intracellular, receptor domain having serine kinase-like  
 CC activity. These proteins have binding affinity for at least one  
 CC member of the activin/TGF-beta superfamily of polypeptide growth  
 CC factors. The activin receptor proteins of the invention can be  
 CC employed for a variety of therapeutic uses, e.g. to block receptors.  
 CC The presence of the soluble proteins will compete with functional  
 CC ligand for the receptor, preventing the formation of a functional  
 CC receptor-ligand complex, thereby blocking the normal regulatory  
 CC action of the complex. The receptor proteins are useful for the  
 CC diagnosis and therapeutic management of carcinogenesis, wound healing,  
 CC disorders of the immune, reproductive, or central nervous systems.

XX Sequence 510 AA;

Query Match 71.2%; Score 1971.5; DB 23; Length 510;  
 Best Local Similarity 67.9%; Pred. No. 1.7e-190;  
 Matches 349; Conservative 85; Mismatches 75; Indels 5; Gaps 3;

QY 1 MGAALAFVFLISCSGAILGRSETQCLFFNANNEKDRNTOTGVEPCYGDKRRHC 60  
 DB 1 MGASVALFTLLLATFRAGSGHDEVETRECIYNNANNELEKTNQSGVESGEKDKRLHC 60  
 QY 61 FATWKNISGSIEIVKQGCWLDIDNCYDRTCVCKKDSPEVYFCCCEGNCNEKFSYFPEM 120  
 DB 61 YASWRNNSGFIELYKGCWLDIDNCYDRQECIAKEENPQVFCCCEGNYCNKKFTLPEV 120  
 QY 121 EYQTSTNPVTPKPPYNNILSYLPLMLIAGIVICAFWYRHHKMAPPPVLVPTQDGP 180  
 DB 121 ETFDPKPQ---PSASVLNLIYSLPIVGLSMAILLAFWMYRHRKPPYGHVEI-NEDPGL 176  
 QY 181 PPSPLGLKPLQLLEKARFGVCWKAQLLNEYVAVKIPIDQKOSQWNEYEVYSLPG 240  
 DB 177 PPSPLVGLKPLQLLEIKARFGVCWKAQLLNEYVAVKIPVQDKSQWQCEKEFTTTPG 236  
 QY 241 MKHENILOFIGAERKGTSDVDMLITAFHEKGSLSDFLKNVYSWNLCHIAETMARGL 300  
 DB 237 MKHENLEFIAAEKGSNLEMLITAFHDKGSITDYLKGNLYSWNLCHITETMARGL 296  
 QY 301 AYLHEDIPGLK-DGHPKPAISHRDIKSNVLLKNNLTACIADFLGALKPEAGKSAGDTHGQ 359  
 DB 297 AYLHEDVPKCGEGHKPAIAHRDFKSNVLLNNDUTAILADFLGLAVREPCKPPGDTHGQ 356  
 QY 360 VGTTRYMAPEVLEGAINFQDAFLRIDMYAMGLVLWELASRCTAAGDPVDEYMLPFEEI 419  
 DB 357 VGTTRYMAPEVLEGAINFQDSFLRIDMYAMGLVLWEIVSRCTAAGDPVDEYMLPFEEI 416  
 QY 420 GQHPSLDQEVVVKRRPVRDYTWQKAGMAMLCETIEECWDHDAEARLSAGCVGRI 479  
 DB 417 GQHPSLDQEVVVKRRPVRDYTWQKAGMAMLCETIEECWDHDAEARLSAGCVGRI 476  
 QY 480 TQWORTNLITTEDIVTVVTNVDFFPKESL 513  
 DB 477 SQIRKSVNGTSDCLSVISVITNVDLPKKESS 510

RESULT 13

AA014119  
 ID AA014119 standard; Protein; 510 AA.

XX AC AA014119;

XX DT 07-MAY-2002 (first entry)

XX DE Protein of a Xenopus-derived activin receptor.

XX

KW Activin receptor; cloning; recombinant; TGF-beta; ligand-binding;  
 KW superfamily; trans-membrane; receptor domain; serine kinase; diagnosis;  
 KW therapeutic management; carcinogenesis; wound healing; protein therapy;  
 KW immune; reproductive; central nervous system; activin-dependent tumour;  
 KW brain neuron; abortion; livestock; twinning; probe; agonist; cytostatic;  
 KW wound healing; transplant organ rejection; vulnery; immunosuppressive;  
 KW transforming growth factor-beta; amphibian.

XX Xenopus sp.

XX US2001039036-A1.

XX 08-NOV-2001.

XX 19-DEC-2000; 2000US-0742684.

XX 07-JUN-1995; 95US-0476123.

XX 08-MAY-1992; 92US-0880220.

XX 10-MAY-1991; 91US-0698709.

XX 09-OCT-1991; 91US-0773229.

XX 02-SEP-1994; 94US-0300584.

XX (SALK ) SALK INST BIOLOGICAL STUDIES.

XX Mathews LS, Vale WW, Tsuchida K;

XX WPI; 2002-040721/05.

XX N-PSDB; AAK98721.

XX New receptor proteins having an extracellular ligand-binding domain, a  
 PT hydrophobic trans-membrane domain, and an intracellular receptor  
 PT domain, useful for diagnosing or treating carcinogenesis, wound healing  
 PT or immune disorders -

XX Claim 5; Page 19-20; 33pp; English.

XX This sequence represents the protein of a Xenopus-derived activin  
 CC receptor. The invention relates to cloning and recombinant production of  
 CC receptor(s) of the activin/TGF-beta (transforming growth factor-beta)  
 CC superfamily. The invention has identified and characterised members of a  
 CC new superfamily of receptor proteins which comprise three distinct  
 CC domains: an extracellular, ligand-binding domain, a hydrophobic, trans-  
 CC membrane domain, and an intracellular, receptor domain having serine  
 CC kinase-like activity. The receptor proteins and antibodies to these  
 CC proteins are useful in the diagnosis and therapeutic management of  
 CC carcinogenesis, wound healing, disorders of the immune, reproductive, or  
 CC central nervous systems. The receptor proteins of the invention can be  
 CC used in protein therapy. These may further be used to diagnose or treat  
 CC activin-dependent tumours, enhance the survival of brain neurons, induce  
 CC abortion in livestock and other domesticated animals, and induce twinning  
 CC in livestock and other domesticated animals. The DNAs are useful as  
 CC probes for identifying additional members of the superfamily of receptor  
 CC proteins, and as coding sequences which can be used for the recombinant  
 CC expression of the receptor proteins. Agonists for TGF-beta specific  
 CC receptors can be used to stimulate wound healing, to suppress growth of  
 CC TGF-beta sensitive tumours, or to suppress immune response (thus prevent  
 CC rejection of transplant organ). The receptor proteins of the invention  
 CC have cytostatic, vulnery, and immunosuppressive activity.

XX Sequence 510 AA;

Query Match 71.2%; Score 1971.5; DB 23; Length 510;  
 Best Local Similarity 67.9%; Pred. No. 1.7e-190;  
 Matches 349; Conservative 85; Mismatches 75; Indels 5; Gaps 3;

QY 1 MGAALAFVFLISCSGAILGRSETQCLFFNANNEKDRNTOTGVEPCYGDKRRHC 60  
 DB 1 MGASVALFTLLLATFRAGSGHDEVETRECIYNNANNELEKTNQSGVESGEKDKRLHC 60

QY 61 FATWKNISGSIEIVKQGCWLDIDNCYDRTCVCKKDSPEVYFCCCEGNCNEKFSYFPEM 120  
 DB 61 YASWRNNSGFIELYKGCWLDIDNCYDRQECIAKEENPQVFCCCEGNYCNKKFTLPEV 120

Qy 121 EVTQTSNPVTPKPPYYNLLYSLVPLMLIAGIVICAFWYVYRHHKMAYPVLPVTPDQGP 180  
 Db 121 ETEDPKPQ---PSASVLNLLIYSLLPVGLSMALLAFWYRHHKPPYGHVEI-NEDPGL 176  
 Qy 181 PPSPLGLKPLQLLEVKARGCGVWKAQLLNEYVAVKIFPIQDKOSQWNEYEYVSLPG 240  
 Db 177 PPSPLVGLKPLQLLEIKARGCGVWKAQLLNEYVAVKIFPIQDKOSQWCEKEIFTTPG 236  
 Qy 241 MKHENILQFAGKRGTSVDVDLWLTAFHEKGSLSDFLKVANVSNOLCHIAETMARGL 300  
 Db 237 MKHENLEFIAAERKGSNLEMLWLTAFHDKGSLDYLKGNLVSNWELCHITETMARGL 296  
 Qy 301 AYLEDIPGLK-DGHKPAISHRDIKSNVLLKNNLTACIADFLGALKFEAGKSAGDTHGQ 359  
 Db 297 AYLEDVPRCKGEGHKAIAHDFKSKNVLRLNDLTAILADFLGAVRFPCKPGDTHGQ 356  
 Qy 360 VGTTRYMAPEVLEGAINFORDAFLRIDMYAMGLVILWELASRCTAADGPVDEYMLPFEEI 419  
 Db 357 VGTTRYMAPEVLEGAINFORDSFLRIDMYAMGLVILWELASRCTAADGPVDEYMLPFEEI 416  
 Qy 420 GOHPSLEDQEVVYVHKRPVLDYVWQKHAGMAMLCETIECDWDHDAEARLSAGCVGERI 479  
 Db 417 GOHPSLEDQEVVYVHKRPVLDYVWQKHAGMAMLCETIECDWDHDAEARLSAGCVGERI 476  
 Qy 480 TOMORLNTIITTEDIVVTVMVTVNDFPKKESL 513  
 Db 477 SQIRKSVNGTSDCLVSIVTSVTNVDLPKKESSI 510

RESULT 14  
 AAR29582  
 ID AAR29582 standard; Protein; 510 AA.  
 AC AAR29582;  
 DT 19-APR-1993 (first entry)  
 DE Xenopus activin receptor.  
 KW Activin receptor; mouse; Xenopus; human; extracellular; ligand binding;  
 KW hydrophobic; trans-membrane; intracellular; receptor; domain;  
 KW serine kinase-like; activity; probe; superfamily; secretion signal;  
 KW golgi membrane; diagnosis; treatment; activin-dependent tumour; brain;  
 KW neuron; abortion; twinning; wound healing; TGF-beta; immune response;  
 KW liver regeneration.  
 XS Xenopus laevis.  
 PN WO9220793-A.  
 XX  
 XX 26-NOV-1992.  
 PD  
 XX 08-MAY-1992; 92WO-US03825.  
 PF  
 XX 10-MAY-1991; 91US-0698709.  
 PR  
 XX 09-OCT-1991; 91US-0773229.  
 XX  
 PA (SALK ) SALK INST BIOLOGICAL STUDIES.  
 XX  
 XX Mathews LS, Vale WW;  
 DR WPI: 1992-415771/50.  
 DR N-PSDB; AAQ31911.  
 XX  
 PT New member of activin-transforming growth factor beta  
 PT super-family - for diagnosis and treatment of cancer and  
 PT disorders of the immune, reproductive or central nervous system  
 XX  
 PS Disclosure; Page 47-49; 68pp; English.  
 XX  
 CC The sequences given in AAR29581-83 represent activin receptors from  
 CC mouse, Xenopus and human respectively. Each of these proteins  
 CC comprise three distinct domains; an extracellular, ligand binding

CC domain, a hydrophobic, trans-membrane domain and an intracellular,  
 CC receptor domain having serine kinase-like activity. The DNA sequences  
 CC encoding these proteins can be used as probes for the identification  
 CC of additional members of this superfamily of receptor molecules. The  
 CC proteins may further comprise a second hydrophobic domain at the amino  
 CC terminal which comprises a secretion signal sequence which promotes  
 CC the intracellular transport of the initially expressed receptor  
 CC protein across the golgi membrane. These receptor proteins can be  
 CC used to develop agents for the diagnosis and/or treatment of eg.  
 CC activin-dependent tumours, for enhancing the survival of brain  
 CC neurons, for inducing abortion or twinning in livestock, for  
 CC stimulating wound healing, for suppression of growth of TGF-beta  
 CC sensitive tumours, for suppressing immune response, for promoting  
 CC liver regeneration and for stimulating some immune responses.

XX Sequence 510 AA;

Query Match 71.1%; Score 1968.5; DB 13; Length 510;  
 Best Local Similarity 67.7%; Pred. No. 3.5e-190;  
 Matches 348; Conservative 86; Mismatches 75; Indels 5; Gaps 3;

Qy 1 MGAARAKLAFVAVLSCSSGAILGRSETQECLEFFNANWEKRTNQTGVEPCYGDKKRRHC 60  
 Db 1 MGASVALTFLLLATFRAGSGHDEVETRECIYYANWELKTNQSGVSCGEKDKRLHC 60  
 Qy 61 FATWKNISGSEIVKQGCWLDIDYCDRTDCVEKKDSPEVYFCCEGNCMEKESYEPPEM 120  
 Db 61 YASWRNNSGFIELYKKGWLDIDYCDYDQECIAKEENPQVEFCCEGNYCNKRKTHLPEV 120  
 Qy 121 EVTQTSNPVTPKPPYYNLLYSLVPLMLIAGIVICAFWYVYRHHKMAYPVLPVTPDQGP 180  
 Db 121 ETEDPKPQ---PSASVLNLLIYSLLPVGLSMALLAFWYRHHKPPYGHVEI-NEDPGL 176  
 Qy 181 PPSPLGLKPLQLLEVKARGCGVWKAQLLNEYVAVKIFPIQDKOSQWNEYEYVSLPG 240  
 Db 177 PPSPLVGLKPLQLLEIKARGCGVWKAQLLNEYVAVKIFPIQDKOSQWCEKEIFTTPG 236  
 Qy 241 MKHENILQFAGKRGTSVDVDLWLTAFHEKGSLSDFLKVANVSNOLCHIAETMARGL 300  
 Db 237 MKHENLEFIAAERKGSNLEMLWLTAFHDKGSLDYLKGNLVSNWELCHITETMARGL 296  
 Qy 301 AYLEDIPGLK-DGHKPAISHRDIKSNVLLKNNLTACIADFLGALKFEAGKSAGDTHGQ 359  
 Db 297 AYLEDVPRCKGEGHKAIAHDFKSKNVLRLNDLTAILADFLGAVRFPCKPGDTHGQ 356  
 Qy 360 VGTTRYMAPEVLEGAINFORDAFLRIDMYAMGLVILWELASRCTAADGPVDEYMLPFEEI 419  
 Db 357 VGTTRYMAPEVLEGAINFORDSFLRIDMYAMGLVILWELASRCTAADGPVDEYMLPFEEI 416  
 Qy 420 GOHPSLEDQEVVYVHKRPVLDYVWQKHAGMAMLCETIECDWDHDAEARLSAGCVGERI 479  
 Db 417 GOHPSLEDQEVVYVHKRPVLDYVWQKHAGMAMLCETIECDWDHDAEARLSAGCVGERI 476  
 Qy 480 TOMORLNTIITTEDIVVTVMVTVNDFPKKESL 513  
 Db 477 SQIRKSVNGTSDCLVSIVTSVTNVDLPKKESSI 510

RESULT 15

AAR86243  
 ID AAR86243 standard; Protein; 512 AA.  
 XX  
 XX AC AAR86243;  
 XX  
 XX 16-FEB-1999 (first entry)  
 DT  
 XX  
 DE Mouse ActRIIB2 receptor protein.  
 XX  
 KW Bone morphogenetic protein; BMP; BMP receptor kinase; ActRIIB receptor;  
 KW BSK; receptor ligand; drug.  
 XX  
 OS Mus sp.  
 XX

QY 487 NIITTEDIVTVVTVMTNVDFFPKESSL 513  
Db 486 NGTTSDCLVSLVTSVTNVDLLPKESSI 512

Search completed: May 10, 2003, 17:58:58  
Job time : 80 secs

PN WO9852038-A1.  
XX 19-NOV-1998.  
XX 13-MAY-1998; 98WO-US09519.  
XX 16-MAY-1997; 97US-0046768.  
XX (PROC ) PROCTER & GAMBLE CO.  
XX Rosenbaum JS;  
XX WPI; 1999-009930/01.  
XX N-PSDB; AAV71967.  
XX  
XX Screening method using bone morphogenetic protein receptor complex -  
XX which binds to potential drugs, and ActRIIB receptor used in the  
XX complex, also host cells transfected with DNA encoding the complex  
XX  
XX Claim 1; Pages 55-57; 110pp; English.  
XX  
XX This represents a mouse ActRIIB2 receptor protein. This can be used in  
XX the method of the invention of determining whether a compound can bind to  
XX a bone morphogenetic protein (BMP) receptor kinase protein complex. The  
XX method comprises allowing a compound in a sample to bind to the complex,  
XX where the complex is comprised of (i) a BMP; (ii) a BMP receptor kinase  
XX protein (BRK); (iii) an ActRIIB receptor. The method can be used to  
XX determine the concentration of a BMP receptor ligand in a sample by  
XX comparing the binding to a standard curve prepared with known  
XX concentrations of BMP ligand. The method can also be used to determine  
XX whether a test compound produces a signal on binding to a BMP receptor  
XX protein complex. The method is useful for determining whether a ligand,  
XX such as a known or putative drug, can bind to and/or activate the  
XX receptors.  
XX  
XX Sequence 512 AA;  
XX  
XX Query Match 69.9%; Score 1935; DB 20; Length 512;  
XX Best Local Similarity 67.3%; Pred. No. 8.6e-187;  
XX Matches 341; Conservative 88; Mismatches 76; Indels 2; Gaps 2;  
XX  
XX QY 8 AFAYFLISCSGAILGRSETQCLFFNANWEKDRNTQTVGPEYCCGECNMCKEFPPEMEVTOPTS 127  
XX Db 7 ALALWGLSAGRGAEARECIYYNANWELRTNQSLERCEGEQDKRLHCYASWRNS 66  
XX  
XX QY 68 SGTIEIVKQGCWLDIDNCYDTRDCVEKKDSPEVYFCCEGNCMKFSPPEMEVTOPTS 127  
XX Db 67 SGTIEIVKQGCWLDIDNCYDTRDCVEKKDSPEVYFCCEGNCMKFSPPEMEVTOPTS 126  
XX  
XX QY 128 NPVTPKPPYYNLLYSLVPLMLIAGIVICAFWYVYRHKKMAYPPVLPVTPDGPDPSPPL 187  
XX Db 127 EPPPTAPTLLTAVLAYSLPIGGLSLIIVLLAFWYVYRHKKMAYPPVLPVTPDGPDPSPPL 185  
XX  
XX QY 188 GLKPLQLLEVKARGFCGCVKQNLINVEYVAFIPIDQKQWQNEVEYISLPGMKHENIL 247  
XX Db 186 GLKPLQLLEVKARGFCGCVKQNLINVEYVAFIPIDQKQWQNEVEYISLPGMKHENIL 245  
XX  
XX QY 248 QFIGAERKRTSVVDLWLITAFHEKGSLSDFLKANVYSWNLCHIAETMARGLAYLHEDI 307  
XX Db 246 QFIAEKRGSNLEVLWLTITAFHDKGSLTDYLGKNIITWNLCHVAETMSRGLSYLHEDV 305  
XX  
XX QY 308 PGLK-DGHHKPAISHRDIKSNVLLKNNLTACIADFGALKEAGKSAGDTHGQVGTTRYM 366  
XX Db 306 PWCGRGEGHKPSIAHRDFKSNVLLKSDLTAVLADFGALKEAGKSAGDTHGQVGTTRYM 365  
XX  
XX QY 367 APEVLEGAINFORDAFLRIDYAMGLVWELASRCTAADGPVDEYMLPFEEIGQHPSPLE 426  
XX Db 366 APEVLEGAINFORDAFLRIDYAMGLVWELASRCTAADGPVDEYMLPFEEIGQHPSPLE 425  
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XX QY 427 DMQEVVHHKKRPVLYRQKQWAGMAMLCETIEECWDHDAEARLSAGCVGERITQMORLT 486  
XX Db 426 ELQEVVHHKKRPVLYRQKQWAGMAMLCETIEECWDHDAEARLSAGCVGERITQMORLT 485

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: May 10, 2003, 17:57:45 ; Search time 24 Seconds  
(without alignments)  
1967.050 Million cell updates/sec

Title: US-09-742-684A-16  
Perfect score: 2770  
Sequence: 1 MGAANKLAFVFLISCSGA.....IVTVVTMTNVDPKESL 513

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 349150 seqs, 92025710 residues

Total number of hits satisfying chosen parameters: 349150

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pcp.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pcp.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pcp.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pcp.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pcp.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pcp.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pcp.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pcp.\*
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- 10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pcp.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pcp.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pcp.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pcp.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match % | Length | ID | Description       |
|------------|--------|---------------|--------|----|-------------------|
| 1          | 2763   | 99.7          | 513    | 10 | US-09-742-684-2   |
| 2          | 1971.5 | 71.2          | 510    | 10 | US-09-742-684-4   |
| 3          | 1150.5 | 41.5          | 516    | 9  | US-10-108-605-79  |
| 4          | 1147.5 | 41.4          | 516    | 9  | US-10-108-605-157 |
| 5          | 775.5  | 28.0          | 567    | 10 | US-09-878-905-11  |
| 6          | 775.5  | 28.0          | 592    | 9  | US-09-917-788-5   |
| 7          | 775.5  | 28.0          | 1038   | 10 | US-09-908-500A-2  |
| 8          | 681    | 24.6          | 1080   | 10 | US-09-904-380-2   |
| 9          | 674    | 24.3          | 532    | 9  | US-09-982-543A-6  |
| 10         | 674    | 24.3          | 532    | 9  | US-10-153-217-2   |
| 11         | 674    | 24.3          | 532    | 10 | US-09-903-068-6   |
| 12         | 669    | 24.2          | 532    | 10 | US-09-903-068-14  |
| 13         | 664    | 24.0          | 532    | 10 | US-09-874-628-2   |
| 14         | 653.5  | 23.6          | 502    | 9  | US-10-044-716-14  |
| 15         | 653.5  | 23.6          | 502    | 10 | US-09-874-628-4   |
| 16         | 647.5  | 23.4          | 502    | 9  | US-09-982-543A-8  |
| 17         | 647.5  | 23.4          | 502    | 10 | US-09-903-068-18  |
| 18         | 643.5  | 23.2          | 493    | 9  | US-09-069-228-2   |
| 19         | 637.5  | 23.0          | 493    | 10 | US-09-742-684-12  |

|    |       |      |     |    |                    |                   |
|----|-------|------|-----|----|--------------------|-------------------|
| 20 | 624   | 22.5 | 503 | 10 | US-09-903-068-10   | Sequence 10, Appl |
| 21 | 622.5 | 22.5 | 503 | 10 | US-09-874-628-10   | Sequence 10, Appl |
| 22 | 615.5 | 22.2 | 505 | 10 | US-09-903-068-8    | Sequence 8, Appl  |
| 23 | 613.5 | 22.1 | 505 | 10 | US-09-771-161A-200 | Sequence 200, App |
| 24 | 606.5 | 21.9 | 505 | 10 | US-09-903-068-16   | Sequence 16, Appl |
| 25 | 606.5 | 21.9 | 505 | 10 | US-09-874-628-8    | Sequence 8, Appl  |
| 26 | 587.5 | 21.2 | 509 | 9  | US-09-982-543A-4   | Sequence 4, Appl  |
| 27 | 587.5 | 21.2 | 509 | 9  | US-10-005-228-2    | Sequence 2, Appl  |
| 28 | 587.5 | 21.2 | 509 | 10 | US-09-903-068-4    | Sequence 4, Appl  |
| 29 | 576   | 20.8 | 503 | 9  | US-09-982-543A-2   | Sequence 2, Appl  |
| 30 | 576   | 20.8 | 503 | 9  | US-10-005-228-4    | Sequence 4, Appl  |
| 31 | 576   | 20.8 | 503 | 10 | US-09-903-068-2    | Sequence 2, Appl  |
| 32 | 575.5 | 20.8 | 509 | 10 | US-09-874-628-6    | Sequence 6, Appl  |
| 33 | 549   | 19.8 | 502 | 10 | US-09-903-068-12   | Sequence 12, Appl |
| 34 | 346   | 12.5 | 139 | 10 | US-09-205-658-20   | Sequence 20, Appl |
| 35 | 346   | 12.5 | 139 | 10 | US-09-844-353A-20  | Sequence 20, Appl |
| 36 | 316   | 11.4 | 198 | 10 | US-09-925-302-500  | Sequence 500, App |
| 37 | 291.5 | 10.5 | 518 | 10 | US-09-771-161A-231 | Sequence 231, App |
| 38 | 282.5 | 10.2 | 497 | 10 | US-09-862-027-8    | Sequence 8, Appl  |
| 39 | 280   | 10.1 | 478 | 9  | US-09-866-050A-512 | Sequence 512, App |
| 40 | 274   | 9.9  | 460 | 9  | US-10-001-254-16   | Sequence 16, App  |
| 41 | 274   | 9.9  | 460 | 9  | US-09-759-595-1    | Sequence 1, Appl  |
| 42 | 270.5 | 9.8  | 460 | 9  | US-10-001-254-28   | Sequence 28, Appl |
| 43 | 268   | 9.7  | 459 | 9  | US-09-759-595-3    | Sequence 3, Appl  |
| 44 | 265.5 | 9.6  | 825 | 9  | US-10-101-464A-922 | Sequence 922, App |
| 45 | 262   | 9.5  | 277 | 9  | US-10-172-088-6    | Sequence 6, Appl  |

ALIGNMENTS

RESULT 1  
US-09-742-684-2  
; Sequence 2, Application US/09742684  
; Patent No. US20010039036A1  
; GENERAL INFORMATION:  
; APPLICANT: Mathews, Lawrence S.  
; Tsuchida, Kunihiko  
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF  
; RECEPTOR(S) OF THE ACTIVIN/TGF-BETA SUPERFAMILY  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09742,684  
FILING DATE: 19-Dec-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/476,123  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/300,584  
FILING DATE: 02-SEP-1994  
APPLICATION NUMBER: US 07/880,220  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: US 07/773,229  
FILING DATE: 09-OCT-1991  
APPLICATION NUMBER: US 07/698,709  
FILING DATE: 10-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P41 9927

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-546-4737

TELEFAX: 619-546-9392

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 513 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-742-684-2

Query Match 99.7%; Score 2763; DB 10; Length 513;

Best Local Similarity 99.4%; Pred. No. 7.9e-218;

Matches 510; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAALKAFVFLISCSGAILGRSETQCLFFNANWEKDRDTNOTGVPCYGDKRRHC 60

DB 1 MGAALKAFVFLISCSGAILGRSETQCLFFNANWEKDRDTNOTGVPCYGDKRRHC 60

QY 61 FATWKNISGSIEIVKQGCWLDINCIDYDTCVEKKDSEVYFCCCEGNCNEKESYFPEM 120

QY 61 FATWKNISGSIEIVKQGCWLDINCIDYDTCIEKKDSEVYFCCCEGNCNEKESYFPEM 120

QY 121 EVTQPTSNPVPKPPYNYLLISLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDGP 180

DB 121 EVTQPTSNPVPKPPYNYLLISLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDGP 180

QY 181 PPPSLGLKPLQLLEVKARGFCVWKQAQLLNEYVAVKFPDQKOSWONEVEYSLPG 240

DB 181 PPPSLGLKPLQLLEVKARGFCVWKQAQLLNEYVAVKFPDQKOSWONEVEYSLPG 240

QY 241 MKHENILQFIGAERKGTSDVDLMLITAFHEKGSLSDFLKVYVSNOLCHIAETMARGL 300

DB 241 MKHENILQFIGAERKGTSDVDLMLITAFHEKGSLSDFLKVYVSNOLCHIAETMARGL 300

QY 301 AYLEDIPGLKDGHPKPAISHRDIKSNVLLKNNLTACIADFGALKFEAGKSAGDTHGQV 360

DB 301 AYLEDIPGLKDGHPKPAISHRDIKSNVLLKNNLTACIADFGALKFEAGKSAGDTHGQV 360

QY 361 GTRRYMAPEVLEGAINFORDAFLRDMYAMGLVWLWELASRCTAADGVPDVEYMLPFEEIG 420

DB 361 GTRRYMAPEVLEGAINFORDAFLRDMYAMGLVWLWELASRCTAADGVPDVEYMLPFEEIG 420

QY 421 QHPSEDMDQEVVYVHKRPVLDYQKQKAGMAMLCETIEECWDHDAEARLSAGCGVERIT 480

DB 421 QHPSEDMDQEVVYVHKRPVLDYQKQKAGMAMLCETIEECWDHDAEARLSAGCGVERIT 480

QY 481 QMRQLTNITTTEDIVVTVMVTNVDFFPKKESL 513

DB 481 QMRQLTNITTTEDIVVTVMVTNVDFFPKKESL 513

RESULT 2

US-09-742-684-4

Sequence 4, Application US/09742684

Patent No. US20010039036A1

GENERAL INFORMATION:

APPLICANT: Mathews, Lawrence S.

Tsuchida, Kunihito

Vale, Wylie W.

TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF

RECEPTOR(S) OF THE ACTIVIN/TGF-BETA SUPERFAMILY

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark

STREET: 444 South Flower Street, Suite 2000

CITY: Los Angeles

STATE: CA

COUNTRY: USA

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/09/742,684

APPLICATION NUMBER: US/09/742,684

FILING DATE: 19-Dec-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/476,123

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/300,584

FILING DATE: 02-SEP-1994

APPLICATION NUMBER: US 07/880,220

FILING DATE: 08-MAY-1992

APPLICATION NUMBER: US 07/773,229

FILING DATE: 09-OCT-1991

APPLICATION NUMBER: US 07/698,709

FILING DATE: 10-MAY-1991

ATTORNEY/AGENT INFORMATION:

NAME: Reiter, Stephen E.

REGISTRATION NUMBER: 31,192

REFERENCE/DOCKET NUMBER: P41 9927

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-546-4737

TELEFAX: 619-546-9392

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 510 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-742-684-4

Query Match 71.2%; Score 1971.5; DB 10; Length 510;

Best Local Similarity 67.9%; Pred. No. 4.2e-153;

Matches 349; Conservative 85; Mismatches 75; Indels 5; Gaps 3;

QY 1 MGAALKAFVFLISCSGAILGRSETQCLFFNANWEKDRDTNOTGVPCYGDKRRHC 60

DB 1 MGAASVALTELLLLATFRAGSGHDEVTRECIYVNNANWELEKTNQSGVESCEGEKRLHC 60

QY 61 FATWKNISGSIEIVKQGCWLDINCIDYDTCVEKKDSEVYFCCCEGNCNEKESYFPEM 120

DB 61 YASWRNNSGFIELVKKGCWLDINCIDYDTCVEKKDSEVYFCCCEGNCNEKESYFPEM 120

QY 121 EVTQPTSNPVPKPPYNYLLISLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDGP 180

DB 121 EYFDPRQ---PSASVNLIIYSLLPVGLSMAILAFWYRHHKPPYGHVEI-NEDPGL 176

QY 181 PPPSLGLKPLQLLEVKARGFCVWKQAQLLNEYVAVKFPDQKOSWONEVEYSLPG 240

DB 177 PPPSLVGLKPLQLLEIKARGFCVWKQAQLLNEYVAVKFPDQKOSWONEVEYSLPG 236

QY 241 MKHENILQFIGAERKGTSDVDLMLITAFHEKGSLSDFLKVYVSNOLCHIAETMARGL 300

DB 237 MKHENLEFIAAEKRGSLNEMELWLITAFHDGSLTDYLLKGLVSNELCHITETMARGL 296

QY 301 AYLEDIPGLK-DGHPKPAISHRDIKSNVLLKNNLTACIADFGALKFEAGKSAGDTHGQ 359

DB 297 AYLEDVPRCKEGEGHPKPAISHRDIKSNVLLKNNLTACIADFGALKFEAGKSAGDTHGQ 356

QY 360 VSTRRYMAPEVLEGAINFORDAFLRDMYAMGLVWLWELASRCTAADGVPDVEYMLPFEEI 419

DB 357 VSTRRYMAPEVLEGAINFORDAFLRDMYAMGLVWLWELASRCTAADGVPDVEYMLPFEEI 416

QY 420 QHPSEDMDQEVVYVHKRPVLDYQKQKAGMAMLCETIEECWDHDAEARLSAGCGVERI 479

DB 417 QHPSEDMDQEVVYVHKRPVLDYQKQKAGMAMLCETIEECWDHDAEARLSAGCGVERI 476

QY 480 TOMQLTNITTTEDIVVTVMVTNVDFFPKKESL 513

DB 477 SQIRKSVNGTTSCLIVSIYTSVTNVDLPKESSI 510

## RESULT 3

US-10-108-605-79  
 ; Sequence 79, Application US/10108605  
 ; Patent No. US20020160934A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Broadus, Julie  
 ; APPLICANT: Stam, Lynn  
 ; APPLICANT: Bachmann, Jane  
 ; APPLICANT: Kamdar, Kim  
 ; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE  
 ; TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF  
 ; FILE REFERENCE: 31133B  
 ; CURRENT APPLICATION NUMBER: US/10/108,605  
 ; CURRENT FILING DATE: 2002-03-27  
 ; PRIOR APPLICATION NUMBER: US 09/761,142  
 ; PRIOR FILING DATE: 2001-01-16  
 ; PRIOR APPLICATION NUMBER: US 60/176,418  
 ; PRIOR FILING DATE: 2000-01-14  
 ; NUMBER OF SEQ ID NOS: 361  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 79  
 ; LENGTH: 516  
 ; TYPE: PRF  
 ; ORGANISM: Drosophila melanogaster  
 US-10-108-605-79

Query Match 41.5%; Score 1150.5; DB 9; Length 516;  
 Best Local Similarity 47.2%; Pred. No. 6e-86;  
 Matches 249; Conservative 83; Mismatches 152; Indels 43; Gaps 17;  
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 Db 11 AQLTVCCLLIGHGSLPGSHGIECEHFD---EKMNTTQOCETRIEHCMEADKFPSCYV 67  
 QY 61 FATW--KNISGSIEIVKQGCWLDINCVDYDTCVEKKDSPE--VYFCCEGNCMEKESYFP 116  
 Db 68 YVLSVNETGTILRMKMCCEFTDMHEC--NOTECVTSAPROGNIHFCCCKGRCSNOKYK 126  
 QY 117 FPE-----MEVYQPTSNPTPKPPYNYLLSLVPLMLIAGIVICAFVYVRRHKMA 167  
 Db 127 IKSTTEATQVPKEKTQGSNLIY---IYIGTSVFSV--LMVIVGM---GLLLYRRRQKA 178  
 QY 168 YPVLVPTQDPPPPSPILLGLKPLQLLEVKARGFGCVWKAQLLNEYVAVKIFPIODKQ 227  
 Db 179 HENE-IPTHEAEITNSPILLSNRPIQLLEQKASGRFGDVWQAKLNQDVAVKIFRMQKE 237  
 QY 228 SHQNEYEYVSLPGMKHENILQFIGAERKGTSDV--VDMLITAFHEKGSLSDFLKANVVS 286  
 Db 238 SWTTEHDYKLPFRMRHPNILEFLGVEKH---MDKPEYWLSTYQHNGSLCDYLKSHTSW 294  
 QY 287 NOLCHIAETMARGLAYLHEDIPGLK-DGHKPAISHRDITKSNVLLKNLTIACIADFG 345  
 Db 295 PELCIAESMANGLAHLHEEIPASKTDGLKPSIAHRDFKSNVLLKSDLTACIADFG 354  
 QY 346 KFEAGKSAGDTHGQVGTTRYMAPEVELEGAINFQDAFLRIDMYAMGLVWELASRCTA 405  
 Db 355 IFQPKPCGDTHGQVGTTRYMAPEVELEGAINFNDAFLRIDVYACGLVWELASRCTDFA 413  
 QY 406 GPVDEYMLPFEEIQHPSLEDMQEVVYVHKRRVLDYVWOKHAGMAMLCETIEECWDH 465  
 Db 414 GPVGEFQLPFAELGLRSLDEQESVYVWKLRPRLLSNRAHPLGCVNFDCTMEECWDH 473  
 QY 466 AEARLSACVGERITQMRITNIITTEDIVTVMTNVDFPPPKSS 512  
 Db 474 AEARLSSCVMERFAQLNKYPS-----TQLLIKHTNID-DAKEST 513

## RESULT 4

US-10-108-605-157  
 ; Sequence 157, Application US/10108605  
 ; Patent No. US20020160934A1

## ; GENERAL INFORMATION:

; APPLICANT: Broadus, Julie  
 ; APPLICANT: Stam, Lynn  
 ; APPLICANT: Bachmann, Jane  
 ; APPLICANT: Kamdar, Kim  
 ; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE  
 ; TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF  
 ; FILE REFERENCE: 31133B  
 ; CURRENT APPLICATION NUMBER: US/10/108,605  
 ; CURRENT FILING DATE: 2002-03-27  
 ; PRIOR APPLICATION NUMBER: US 09/761,142  
 ; PRIOR FILING DATE: 2001-01-16  
 ; PRIOR APPLICATION NUMBER: US 60/176,418  
 ; PRIOR FILING DATE: 2000-01-14  
 ; NUMBER OF SEQ ID NOS: 361  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 157  
 ; LENGTH: 516  
 ; TYPE: PRF  
 ; ORGANISM: Drosophila melanogaster  
 US-10-108-605-157

Query Match 41.4%; Score 1147.5; DB 9; Length 516;  
 Best Local Similarity 47.8%; Pred. No. 1.1e-85;  
 Matches 251; Conservative 83; Mismatches 144; Indels 47; Gaps 19;  
 QY 11 VFLISC---SSGAIL-CRSETQCLFFNANWEK--DRTNQ--TGVEPCYGDKRRHCFA 62  
 Db 13 VTLVCCLLIGHGSLPGSHGIECEHFD---EKMNTTQOCETRIEHCMEADKFPSCYV 69  
 QY 63 TW--KNISGSIEIVKQGCWLDINCVDYDTCVEKKDSPE--VYFCCEGNCMEKESYFP 118  
 Db 70 LWSVNETGTILRMKMCCEFTDMHEC--NOTECVTSAPROGNIHFCCCKGRCSNOKYK 128  
 QY 119 E-----MEVYQPTSNPTPKPPYNYLLSLVPLMLIAGIVICAFVYVRRHKMAYP 169  
 Db 129 STTEATQVPKEKTQGSNLIY---IYIGTSVFSV--LMVIVGM---GLLLYRRRQKAHF 180  
 QY 170 PVLVPTQDPPPPSPILLGLKPLQLLEVKARGFGCVWKAQLLNEYVAVKIFPIODKQSW 229  
 Db 181 NE-IPTHEAEITNSPILLSNRPIQLLEQKASGRFGDVWQAKLNQDVAVKIFRMQKESW 239  
 QY 230 QNEYEYVSLPGMKHENILQFIGAERKGTSDV--VDMLITAFHEKGSLSDFLKANVVS 288  
 Db 240 TTEHDYKLPFRMRHPNILEFLGVEKH---MDKPEYWLSTYQHNGSLCDYLKSHTSW 296  
 QY 289 LCHIAETMARGLAYLHEDIPGLK-DGHKPAISHRDITKSNVLLKNLTIACIADFG 347  
 Db 297 LCRIAESMANGLAHLHEEIPASKTDGLKPSIAHRDFKSNVLLKSDLTACIADFG 356  
 QY 348 EAGKSAGDTHGQVGTTRYMAPEVELEGAINFQDAFLRIDMYAMGLVWELASRCTA 407  
 Db 357 QPKPCGDTHGQVGTTRYMAPEVELEGAINFNDAFLRIDVYACGLVWELASRCTDFA 415  
 QY 408 VDEYMLPFEEIQHPSLEDMQEVVYVHKRRVLDYVWOKHAGMAMLCETIEECWDH 467  
 Db 416 VGEFQLPFAELGLRSLDEQESVYVWKLRPRLLSNRAHPLGCVNFDCTMEECWDH 475  
 QY 468 AEARLSACVGERITQMRITNIITTEDIVTVMTNVDFPPPKSS 512  
 Db 476 AEARLSSCVMERFAQLNKYPS-----TQLLIKHTNID-DAKEST 513

## RESULT 5

US-09-878-905-11  
 ; Sequence 11, Application US/09878905  
 ; Patent No. US20020064786A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Markowitz, Sanford D  
 ; APPLICANT: Brattain, Michael G  
 ; APPLICANT: Willson, James K.V.  
 ; TITLE OF INVENTION: CANCER DIAGNOSIS, PROGNOSIS AND THERAPY BASED ON  
 ; TITLE OF INVENTION: MUTATION OF RECEPTOR

[illegible]



[illegible]

RESULT 9  
IIS-09-982-543A-6

US-09-982-543A-b  
 , Sequence 6, Application US/09982543A  
 , Patent No. US20020155500A1  
 , GENERAL INFORMATION:  
 , APPLICANT: Djike, P.  
 , APPLICANT: Miyazano, K.  
 , APPLICANT: Sampath, K.  
 , APPLICANT: Heldin, C.  
 , TITLE OF INVENTION: MORPHOGENIC PROTEIN-SPECIFIC CELL SURFACE RECEPTORS AND USES  
 , TITLE OF INVENTION: THEREFOR  
 , FILE REFERENCE: CIBT-P04-543  
 , CURRENT APPLICATION NUMBER: US/09/982,543A  
 , CURRENT FILING DATE: 2001-10-18  
 , PRIOR APPLICATION NUMBER: 08/448,371  
 , PRIOR FILING DATE: 1995-06-02  
 , NUMBER OF SEQ ID NOS: 15  
 , SOFTWARE: PatentIn version 3.1  
 , SEQ ID NO 6  
 , LENGTH: 532  
 , TYPE: PRT  
 , ORGANISM: Homo sapiens  
 US-09-982-543A-6

|                       |              |                    |                 |             |
|-----------------------|--------------|--------------------|-----------------|-------------|
| Query Match           | 24.3%        | Score 674;         | DB 9;           | Length 532; |
| Best Local Similarity | 34.4%;       | Pred. No. 5.8e-47; |                 |             |
| Matches 164;          | Conservative | 86;                | Mismatches 159; | Indels 68;  |
|                       |              |                    |                 | Gaps 15;    |

|    |     |  |     |
|----|-----|--|-----|
| QY | 59  | HCFATWKNITSGSTEIVKQGCGWLDDINCYDRTDCVEKKDSPEVYFC-----CCGECNMCNEKF | 114 |
| Db | 81  | HCFALIEEDDOGETTTLASGMK-----YEGSD-FQCCKSPKAQLRRRTIECCRTNLCN----   | 131 |
| QY | 115 | SYFPEMEVTQTSNPVTPPPY-----YNLLIYSLVPLMLIAGIVICAEFWVRHH-----       | 164 |
| Db | 132 | -----QYLOPTLPVPVIGFFDGSTRWLVLISMA-VCLIAMIISSFCFYKHCKSTS          | 184 |
| QY | 165 | -----KMAYPPV-----LVPTQDPGPPPSPLL-----LKPLQLLEVKRGR               | 202 |
| Db | 185 | SRRRYNRDLQEDEAFIPVGESLKDLDQSOGSSGGSLPLLVRTAKOIQVMRVQVKGR         | 244 |
| QY | 203 | FGCWKAQALLNEYAVNKIPIQDKSQWONEYEYVYLPGMKHENILOFIGAEKRGTSDVDV      | 262 |
| Db | 245 | YGVEWMGKWGEKVAKVVFVFTTBESWFRETEIYQVLMRHNILGFIAADIKGTGSWTQ        | 304 |
| QY | 263 | LWLITAFHEKSGLSDFLKANVWSWNOLCHTAETMARGLAYLHEDIPLGDGHKPATSHRD      | 322 |
| Db | 305 | LYLITDYHENGSLYDFLKCATLDTFRALLKLAYSAAACGLCHLHFYYGTGC--KPAIAHRD    | 362 |
| QY | 323 | IKSNVLLLNLTACIADFGLALKFBAGKSAGDT--HGQVGTGRRYMAPEVLEGAIN---F      | 377 |

|                           |        |                  |            |              |
|---------------------------|--------|------------------|------------|--------------|
| Query Match               | 24.6%  | Score 681;       | DB 10;     | Length 1080; |
| Best Local Similarity     | 34.0%; | Pred. No. 4e-47; |            |              |
| Matches 181; Conservative | 97;    | Mismatches 173;  | Indels 82; | Gaps 29;     |

|    |     |            |                   |                  |                           |     |
|----|-----|------------|-------------------|------------------|---------------------------|-----|
| QY | 11  | VFLISCSGA  | ILGRSETQ          | ---CLFFNANWEKDR  | -----TNOTGVCFYCDKDKRRHC   | -60 |
|    |     | :          | :                 | :                | :                         |     |
| Db | 19  | ILLVSTAAA  | -----SQNERLCCAFDP | QQDGLIGESRISHENG | TILC-----SKGSTCY          | 69  |
|    |     | :          | :                 | :                | :                         |     |
| QY | 61  | FATWKNISGS | IEIVKQG           | -CWL---DDINCYDRD | TEVEKKDSPEV-----YFCCCEGNC | 110 |
|    |     | :          | :                 | :                | :                         |     |
| Db | 70  | YGLWEKSGD  | INLVKQCC          | SHIGDQFECH       | -YEECVVTTTTPPSIQNGTYRFCC  | 128 |
|    |     | :          | :                 | :                | :                         |     |
| QY | 111 | NEKFS      | -YFPEMEV          | TPQTSN           | VPYKPPYYN---ILLYSLVPLML   | 162 |
|    |     | :          | :                 | :                | :                         |     |
| Db | 129 | NVNFTENEP  | -----PPPD         | TTPLSP           | -PHSFNRDETI               | 183 |
|    |     | :          | :                 | :                | :                         |     |
| QY | 163 | -----HHK   | MAYPVL            | VPYTPD           | GPSPPSGLPLQLLE            | 214 |
|    |     | :          | :                 | :                | :                         |     |

Db 363 LKSNLILIKNGSCCADIAGLAWKFNSTNEVDVPLNTRVGTFRYMAPEVLDLSLKNHF 422  
Qy 378 QDAFLRIDMYAGMLVWELASRCTAADGPVDEYMLPFEEETGOHPDSEDMQEVVHKKK 437  
Db 423 Q--PYMADIYSGLLIWEWARCITG-GIVEEYQLPYNNWPSDSYEDMREVVCVKRL 479  
Qy 438 RPLVLDYQKAGMAMLCETIEECWDHDAEARLSAGCVGERITQMORLTNIITEDI 494  
Db 480 RPIVSNRWNSECLRAVLKLMSECAHNPASRLTA-----LRIKKTAKMVESQDV 530  
RESULT 10  
US-10-153-217-2  
; Sequence 2, Application US/10153217  
; Publication No. US20030072758A1  
; GENERAL INFORMATION:  
; APPLICANT: HOWE, JAMES R.  
; TITLE OF INVENTION: BMPRIA INVOLVEMENT IN JUVENILE POLYPOSIS  
; FILE REFERENCE: IOWA:037US  
; CURRENT APPLICATION NUMBER: US/10/153,217  
; CURRENT FILING DATE: 2002-05-21  
; PRIOR APPLICATION NUMBER: 60/292,691  
; PRIOR FILING DATE: 2001-05-21  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 532  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-153-217-2  
Query Match 24.3%; Score 674; DB 9; Length 532;  
Best Local Similarity 34.4%; Pred. No. 5.8e-47;  
Matches 164; Conservative 86; Mismatches 159; Indels 68; Gaps 15;  
Qy 59 HCFATWKNISGIEIVKOGCWLDDINCYDRTDCVEKKDSPEVYFC-----CCEGNCNEKF 114  
Db 81 HCFATIEDDQGETTLASGCMK-----YEGSD-FQCKDSPKALRRTIECCRTNLCN--- 131  
Qy 115 SYFPEMEVTPQTSNPVTPKPPY-----YNILLYSLVPLMLIAGIVICAFWVYRHH----- 164  
Db 132 -----QYLOPTLPVVGFFDGSIRWLVLISMA-VCIAMIIFSSCFCKHYCKSIS 184  
Qy 165 -----KMAYPPV-----LVPTQDPGPPPPSPLLG-----LKPLQLLEVKARGR 202  
Db 185 SRRYNRDLEQDEAFIPVGSGLKDLIDQSSGSGGLPLLQRTIAKQIOMVRQVKGK 244  
Qy 203 FGCWVKAQLLNEYVAVKIFPIQDKQSNQNEYVYSLPGMKHENILOFIGAERKGTSDVD 262  
Db 245 YGEVWNGKRGKAVKVFVFTTEASWFRTEIYQTVLMRHNILGFIADIKGTGWTQ 304  
Qy 263 LWLITAPHEKGSLSDFLKANVSVNQLCHIAETWARGLYLHEDIPGLKDGHPAISHRD 322  
Db 305 LYLITDYHENGSLYDFLKCATLDTALLKLAYSAAACGLHLHTEIYGTG--KPAIAHRD 362  
Qy 323 IKSNNVLLKNNLTACIADFGLALFEAGKSAGDT--HGQVGTTRYMAPEVLEGAIN---F 377  
Db 363 LKSNLILIKNGSCCADIADGLAVKFNSTNEVDVPLNTRVGTFRYMAPEVLDLSLKNHF 422  
Qy 378 QDAFLRIDMYAGMLVWELASRCTAADGPVDEYMLPFEEETGOHPDSEDMQEVVHKKK 437  
Db 423 Q--PYMADIYSGLLIWEWARCITG-GIVEEYQLPYNNWPSDSYEDMREVVCVKRL 479  
Qy 438 RPLVLDYQKAGMAMLCETIEECWDHDAEARLSAGCVGERITQMORLTNIITEDI 494  
Db 480 RPIVSNRWNSECLRAVLKLMSECAHNPASRLTA-----LRIKKTAKMVESQDV 530  
RESULT 11  
US-09-903-068-6  
; Sequence 6, Application US/09903068

; Patent No. US20020123139A1  
; GENERAL INFORMATION:  
; APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;  
; Frautzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik  
; TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins  
; Having Serine Threonine Kinase Domains And Their Use  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York City  
; STATE: New York  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage  
; COMPUTER: IBM  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/903,068  
; FILING DATE: 11-Jul-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/679,187  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: PCT/GB93/02367  
; FILING DATE: 17-No. US20020123139A1ember-1993  
; APPLICATION NUMBER: 9224057.1  
; FILING DATE: 17-No. US20020123139A1ember-1992  
; APPLICATION NUMBER: 9304677.9  
; FILING DATE: 8-March-1993  
; APPLICATION NUMBER: 9304680.3  
; FILING DATE: 8-March-1993  
; APPLICATION NUMBER: 9311047.6  
; FILING DATE: 28-May-1993  
; APPLICATION NUMBER: 9313763.6  
; FILING DATE: 2-July-1993  
; APPLICATION NUMBER: 9136099.2  
; FILING DATE: 3-August-1993  
; APPLICATION NUMBER: 9321344.5  
; FILING DATE: 15-October-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kohlei, Vineet  
; REGISTRATION NUMBER: 37,003  
; REFERENCE/DOCKET NUMBER: LUD 5298  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 688-9200  
; TELEFAX: (212) 838-3884  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 532 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-903-068-6  
Query Match 24.3%; Score 674; DB 10; Length 532;  
Best Local Similarity 34.4%; Pred. No. 5.8e-47;  
Matches 164; Conservative 86; Mismatches 159; Indels 68; Gaps 15;  
Qy 59 HCFATWKNISGIEIVKOGCWLDDINCYDRTDCVEKKDSPEVYFC-----CCEGNCNEKF 114  
Db 81 HCFATIEDDQGETTLASGCMK-----YEGSD-FQCKDSPKALRRTIECCRTNLCN--- 131  
Qy 115 SYFPEMEVTPQTSNPVTPKPPY-----YNILLYSLVPLMLIAGIVICAFWVYRHH----- 164  
Db 132 -----QYLOPTLPVVGFFDGSIRWLVLISMA-VCIAMIIFSSCFCKHYCKSIS 184  
Qy 165 -----KMAYPPV-----LVPTQDPGPPPPSPLLG-----LKPLQLLEVKARGR 202  
Db 185 SRRYNRDLEQDEAFIPVGSGLKDLIDQSSGSGGLPLLQRTIAKQIOMVRQVKGK 244  
Qy 203 FGCWVKAQLLNEYVAVKIFPIQDKQSNQNEYVYSLPGMKHENILOFIGAERKGTSDVD 262





Search completed: May 10, 2003, 18:01:05  
Job time : 26 secs



GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: May 10, 2003, 17:56:45 ; Search time 16 seconds  
(without alignments)  
943.372 Million cell updates/sec

Title: US-09-742-684A-16  
Perfect score: 2770  
Sequence: 1 MGAARKLAFVFLISCSGA.....IVTVVTMTNVDFPKKSSL 513

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2.6/ptodata/1/1aa/5A-COMB.pep:\*  
2: /cgn2.6/ptodata/1/1aa/5B-COMB.pep:\*  
3: /cgn2.6/ptodata/1/1aa/6A-COMB.pep:\*  
4: /cgn2.6/ptodata/1/1aa/6B-COMB.pep:\*  
5: /cgn2.6/ptodata/1/1aa/PCTUS-COMB.pep:\*  
6: /cgn2.6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID | Description       |
|------------|--------|-------------|--------|-------|-------------------|
|            |        |             |        |       |                   |
| 1          | 2763   | 99.7        | 513    | 2     | US-08-357-533A-10 |
| 2          | 2763   | 99.7        | 513    | 2     | US-08-459-009-10  |
| 3          | 2763   | 99.7        | 513    | 2     | US-08-300-584-2   |
| 4          | 2763   | 99.7        | 513    | 3     | US-08-459-951-10  |
| 5          | 2763   | 99.7        | 513    | 4     | US-08-738-168B-13 |
| 6          | 2763   | 99.7        | 513    | 4     | US-08-476-123-2   |
| 7          | 2749   | 99.2        | 521    | 4     | US-08-738-168B-5  |
| 8          | 2482.5 | 89.6        | 514    | 4     | US-08-738-168B-15 |
| 9          | 1971.5 | 71.2        | 510    | 2     | US-08-300-584-4   |
| 10         | 1971.5 | 71.2        | 510    | 2     | US-08-476-123-4   |
| 11         | 1931   | 69.7        | 536    | 2     | US-08-357-533A-12 |
| 12         | 1931   | 69.7        | 536    | 2     | US-08-459-009-12  |
| 13         | 1931   | 69.7        | 536    | 3     | US-08-459-951-12  |
| 14         | 1915.5 | 69.2        | 513    | 2     | US-08-357-533A-11 |
| 15         | 1915.5 | 69.2        | 513    | 2     | US-08-459-009-11  |
| 16         | 1915.5 | 69.2        | 513    | 3     | US-08-459-951-11  |
| 17         | 1702   | 61.4        | 323    | 4     | US-08-158-735A-12 |
| 18         | 1147.5 | 41.4        | 516    | 2     | US-08-357-533A-2  |
| 19         | 1147.5 | 41.4        | 516    | 2     | US-08-459-009-2   |
| 20         | 1147.5 | 41.4        | 516    | 3     | US-08-459-951-2   |
| 21         | 775.5  | 28.0        | 567    | 1     | US-08-361-873A-2  |
| 22         | 775.5  | 28.0        | 567    | 2     | US-08-483-926A-1  |
| 23         | 775.5  | 28.0        | 567    | 2     | US-08-854-768-1   |
| 24         | 775.5  | 28.0        | 567    | 2     | US-08-445-520B-9  |
| 25         | 775.5  | 28.0        | 567    | 2     | US-08-737-045-1   |
| 26         | 775.5  | 28.0        | 567    | 3     | US-08-451-946B-8  |
| 27         | 775.5  | 28.0        | 567    | 3     | US-08-446-938B-8  |

|    |       |      |      |   |                   |                    |
|----|-------|------|------|---|-------------------|--------------------|
| 28 | 775.5 | 28.0 | 567  | 3 | US-08-311-703A-8  | Sequence 8, Appli  |
| 29 | 775.5 | 28.0 | 567  | 3 | US-08-446-938B-8  | Sequence 8, Appli  |
| 30 | 775.5 | 28.0 | 567  | 3 | US-09-183-543-8   | Sequence 8, Appli  |
| 31 | 775.5 | 28.0 | 567  | 4 | US-08-446-936A-8  | Sequence 8, Appli  |
| 32 | 775.5 | 28.0 | 567  | 4 | US-09-239-864A-11 | Sequence 11, Appli |
| 33 | 775.5 | 28.0 | 567  | 5 | PCT-US92-09326-4  | Sequence 4, Appli  |
| 34 | 775.5 | 28.0 | 582  | 4 | US-08-334-179A-4  | Sequence 4, Appli  |
| 35 | 775.5 | 28.0 | 1038 | 4 | US-08-334-179A-2  | Sequence 2, Appli  |
| 36 | 770.5 | 27.8 | 1038 | 4 | US-08-334-179A-8  | Sequence 8, Appli  |
| 37 | 731.5 | 26.4 | 565  | 2 | US-08-357-533A-9  | Sequence 9, Appli  |
| 38 | 731.5 | 26.4 | 565  | 2 | US-08-459-009-9   | Sequence 9, Appli  |
| 39 | 731.5 | 26.4 | 565  | 3 | US-08-459-951-9   | Sequence 9, Appli  |
| 40 | 717.5 | 25.9 | 325  | 4 | US-08-158-735A-13 | Sequence 13, Appli |
| 41 | 674   | 24.3 | 532  | 2 | US-08-481-337A-6  | Sequence 6, Appli  |
| 42 | 674   | 24.3 | 532  | 4 | US-09-382-256-6   | Sequence 6, Appli  |
| 43 | 674   | 24.3 | 532  | 4 | US-09-395-115-6   | Sequence 6, Appli  |
| 44 | 674   | 24.3 | 532  | 4 | US-08-436-265-6   | Sequence 6, Appli  |
| 45 | 674   | 24.3 | 532  | 4 | US-09-679-187-6   | Sequence 6, Appli  |

ALIGNMENTS

RESULT 1  
US-08-357-533A-10  
; Sequence 10, Application US/08357533A  
; Patent No. 5831050  
; GENERAL INFORMATION:  
; APPLICANT: JIN, DONALD F  
; APPLICANT: OPPERMAN, HERMANN  
; APPLICANT: KUBERASAMPATH, THANGAVEL  
; APPLICANT: SMART, JOHN E  
; TITLE OF INVENTION: NOVEL MORPHOGEN CELL SURFACE RECEPTOR  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,  
; STREET: 45 SOUTH STREET  
; CITY: HOPKINTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 01748  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/357,533A  
; FILING DATE: 16-DEC-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KELLY, ROBIN D  
; REGISTRATION NUMBER: 34,637  
; REFERENCE/DOCKET NUMBER: CRP-073FW  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (508)-435-9001  
; TELEFAX: (508)-435-0992  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 513 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..513  
; OTHER INFORMATION: /note= "MOUSE ACTIVIN RECEPTOR"  
US-08-357-533A-10

Query Match 99.7%; Score 2763; DB 2; Length 513;  
Best Local Similarity 99.4%; Pred. No. 6.2e-264;

Matches 510; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MGAAGLAFVFLISCGSAILGRSETQCLFFNANWEDRTNQTGVEPCYGDKDRHRC 60
DB 1 MGAAGLAFVFLISCGSAILGRSETQCLFFNANWEDRTNQTGVEPCYGDKDRHRC 60
QY 61 FATWKNISGSIEIVKQGCWLDINCYDRTDCVEKKDSPEVYFCCCEGNNMCNEKFSYFPEM 120
DB 61 FATWKNISGSIEIVKQGCWLDINCYDRTDCIEKKDSPEVYFCCCEGNNMCNEKFSYFPEM 120
QY 121 EVTQTSNPVTPKPPYNNILLYSLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDGP 180
DB 121 EVTQTSNPVTPKPPYNNILLYSLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDGP 180
QY 181 PPPSLGLKPLQLLEVKARGFCVWKAQLLNEYVAVKIPFIQDKQSWQNEVEYVSLPG 240
DB 181 PPPSLGLKPLQLLEVKARGFCVWKAQLLNEYVAVKIPFIQDKQSWQNEVEYVSLPG 240
QY 241 MKHENILOFIGAERKGTSDVDLWLITAFHEKGSLSDFLKNVYVSNOLCHIAETMARGL 300
DB 241 MKHENILOFIGAERKGTSDVDLWLITAFHEKGSLSDFLKNVYVSNOLCHIAETMARGL 300
QY 301 AYLEDIPGLKDGHPKPAISHRDIKSNVLLKNNLTACIADFGALKEAGKSAGDTHGOV 360
DB 301 AYLEDIPGLKDGHPKPAISHRDIKSNVLLKNNLTACIADFGALKEAGKSAGDTHGOV 360
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DB 361 GTRRYMAPEVLEGAIFQDAFLRIDMYAMGLVWLWELASRCTAAGDPVDEYMLPFEEIG 420
QY 421 QHPSLEDQMEVYVHKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480
DB 421 QHPSLEDQMEVYVHKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480
QY 481 QMORLTNIITTEDIVVTVMVNTVNDVFPKSSSL 513
DB 481 QMORLTNIITTEDIVVTVMVNTVNDVFPKSSSL 513
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RESULT 2

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US-08-459-009-10
; Sequence 10, Application US/08459009
; Patent No. 5861479
; GENERAL INFORMATION:
; APPLICANT: JIN, DONALD F
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: SMART, JOHN E
; TITLE OF INVENTION: NOVEL MORPHOGEN CELL SURFACE RECEPTOR
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,009
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/357,533
; FILING DATE: 16-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLY, ROBIN D
; REGISTRATION NUMBER: 34,637
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REFERENCE/DOCKET NUMBER: CRP-073FW

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; TELEPHONE: (508)-435-9001
; TELEFAX: (508)-435-0992
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 513 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..513
; OTHER INFORMATION: /note= "MOUSE ACTIVIN RECEPTOR"
US-08-459-009-10
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Query Match 99.7%; Score 2763; DB 2; Length 513;

Best Local Similarity 99.4%; Pred. No. 6.2e-264; Mismatches 3; Indels 0; Gaps 0; Matches 510; Conservative 3;

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DB 1 MGAAGLAFVFLISCGSAILGRSETQCLFFNANWEDRTNQTGVEPCYGDKDRHRC 60
QY 61 FATWKNISGSIEIVKQGCWLDINCYDRTDCVEKKDSPEVYFCCCEGNNMCNEKFSYFPEM 120
DB 61 FATWKNISGSIEIVKQGCWLDINCYDRTDCIEKKDSPEVYFCCCEGNNMCNEKFSYFPEM 120
QY 121 EVTQTSNPVTPKPPYNNILLYSLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDGP 180
DB 121 EVTQTSNPVTPKPPYNNILLYSLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDGP 180
QY 181 PPPSLGLKPLQLLEVKARGFCVWKAQLLNEYVAVKIPFIQDKQSWQNEVEYVSLPG 240
DB 181 PPPSLGLKPLQLLEVKARGFCVWKAQLLNEYVAVKIPFIQDKQSWQNEVEYVSLPG 240
QY 241 MKHENILOFIGAERKGTSDVDLWLITAFHEKGSLSDFLKNVYVSNOLCHIAETMARGL 300
DB 241 MKHENILOFIGAERKGTSDVDLWLITAFHEKGSLSDFLKNVYVSNOLCHIAETMARGL 300
QY 301 AYLEDIPGLKDGHPKPAISHRDIKSNVLLKNNLTACIADFGALKEAGKSAGDTHGOV 360
DB 301 AYLEDIPGLKDGHPKPAISHRDIKSNVLLKNNLTACIADFGALKEAGKSAGDTHGOV 360
QY 361 GTRRYMAPEVLEGAIFQDAFLRIDMYAMGLVWLWELASRCTAAGDPVDEYMLPFEEIG 420
DB 361 GTRRYMAPEVLEGAIFQDAFLRIDMYAMGLVWLWELASRCTAAGDPVDEYMLPFEEIG 420
QY 421 QHPSLEDQMEVYVHKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480
DB 421 QHPSLEDQMEVYVHKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480
QY 481 QMORLTNIITTEDIVVTVMVNTVNDVFPKSSSL 513
DB 481 QMORLTNIITTEDIVVTVMVNTVNDVFPKSSSL 513
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RESULT 3

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US-08-300-584-2
; Sequence 2, Application US/08300584
; Patent No. 5885794
; GENERAL INFORMATION:
; APPLICANT: Mathews, Lawrence S.
; APPLICANT: Vale, Wylie W.
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
; TITLE OF INVENTION: RECEPTOR(S) OF THE ACTIVIN/TGF-BETA SUPERFAMILY
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
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COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/300,584  
FILING DATE: 02-SEP-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/880,220  
FILING DATE: 08-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/773,229  
FILING DATE: 09-OCT-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/698,709  
FILING DATE: 10-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P41 9806  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-1995  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 513 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-300-584-2

Query Match 99.7%; Score 2763; DB 2; Length 513;  
Best Local Similarity 99.4%; Pred. No. 6.2e-264;  
Matches 510; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGAALKAFVFLISCGSAILGRSETQCLFFNANWEKDRNTQGTGVEPCYGDKKRRHC 60  
DB 1 MGAALKAFVFLISCGSAILGRSETQCLFFNANWEKDRNTQGTGVEPCYGDKKRRHC 60  
QY 61 FATWKNISGSIEIVKQGCWLDINCYDRTDCIEKKDSPEVYFCCCGNMCNEKFSYFPEM 120  
DB 61 FATWKNISGSIEIVKQGCWLDINCYDRTDCIEKKDSPEVYFCCCGNMCNEKFSYFPEM 120  
QY 121 EVTQPTSNPVTPKPPYYNLLYSVLPLMLIAGIVICAFWYRHHKMAYPVPLVPTQDPGP 180  
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DB 181 PPPSPLGLKPLQLLEVKARGFGCVWKAQLLNEYVAVKIFPIQDKOSQWNEYVYSLPG 240  
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DB 241 MKHENILOFIGAEGKRGTSVDVLDMLITAFHEKGSLSDFLKANYVSNWOLCHIAETMARGL 300  
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DB 421 QHPSLEDQEVVHVKKRPVLDYWKQHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480  
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DB 481 QMORLTNIITIEDIVVTVMVTVNVDPPKSSSL 513  
RESULT 4  
US-08-459-951-10  
Sequence 10, Application US/08459951  
Patent No. 6093547  
GENERAL INFORMATION:  
APPLICANT: JIN, DONALD F  
APPLICANT: OPPERMAN, HERMANN  
APPLICANT: KUBERASAMPATH, THANGAVEL  
APPLICANT: SMART, JOHN E  
TITLE OF INVENTION: NOVEL MORPHOGEN CELL SURFACE RECEPTOR  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,  
ADDRESSEE: INC  
STREET: 45 SOUTH STREET  
CITY: HOPKINTON  
STATE: MA  
COUNTRY: USA  
ZIP: 01748  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,951  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/357,533  
FILING DATE: 16-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: KELLY, ROBIN D  
REGISTRATION NUMBER: 34,637  
REFERENCE/DOCKET NUMBER: CRP-073FW  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (508)-435-9001  
TELEFAX: (508)-435-0992  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 513 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1-513  
OTHER INFORMATION: /note= "MOUSE ACTIVIN RECEPTOR"  
US-08-459-951-10

Query Match 99.7%; Score 2763; DB 3; Length 513;  
Best Local Similarity 99.4%; Pred. No. 6.2e-264;  
Matches 510; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGAALKAFVFLISCGSAILGRSETQCLFFNANWEKDRNTQGTGVEPCYGDKKRRHC 60  
DB 1 MGAALKAFVFLISCGSAILGRSETQCLFFNANWEKDRNTQGTGVEPCYGDKKRRHC 60  
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QY 241 MKHENILQFIGAEKRGTSVDVLDLITAFHEKGSLSDFLKANVVSNNOLCHIAETMARGL 300  
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DB 481 QMORLTNIITTEDIVTVVMTNVDPPKESL 513

RESULT 5

-08-738-168B-13  
; Sequence 13, Application US/08738168B  
; Patent No. 6132988  
; GENERAL INFORMATION:  
; APPLICANT: Sugino, Hiromu  
; APPLICANT: Nakamura, Takanori  
; APPLICANT: Shouji, Hiroki  
; TITLE OF INVENTION: NEURONAL CELL-SPECIFIC RECEPTOR PROTEIN  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/738,168B  
; FILING DATE: 25-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 280939/1995  
; FILING DATE: 27-OCT-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 174909/1996  
; FILING DATE: 04-JUL-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Resnick, David S.  
; REGISTRATION NUMBER: 34,235  
; REFERENCE/DOCKET NUMBER: 342/46901  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 513 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-738-168B-13

Query Match 99.7%; Score 2763; DB 4; Length 513;  
Best Local Similarity 99.4%; Pred. No. 6,2e-264;  
Matches 510; Conservative 3; Mismatches 0; Indels. 0; Gaps 0;  
QY 1 MGAALKAFVFLSCSSGAILGRSETQCLFFNANWEKDRNTQGVPCYGDKDKRRHC 60

DB 1 MGAALKAFVFLSCSSGAILGRSETQCLFFNANWEKDRNTQGVPCYGDKDKRRHC 60  
QY 61 FATWKNISGSIIVKQGCWLDINCYDRTDCVEKKDSPEVYFCCEGNCMEKESYFPEM 120  
DB 61 FATWKNISGSIIVKQGCWLDINCYDRTDCIEKKDSPEVYFCCEGNCMEKESYFPEM 120  
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DB 181 PPPSPLLGLKPLQLLEVARGFGCVKWAQLLNVEYVAVKIPIQDKQSWQNEIYVSLPG 240  
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DB 241 MKHENILQFIGAEKRGTSVDVLDLITAFHEKGSLSDFLKANVVSNNELCHIAETMARGL 300  
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DB 301 AYLEDIPGLKDGHPKPAISHRDIKSNVLLKNNLTACIADFGALAKFEAGKSAGDTHGQV 360  
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DB 361 GTRRYMAPEVLEGAINFORDAFLRDMYAMGLVWLWELASRCTAAGDPVDEYMLPFEIEIG 420  
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DB 421 QHPSLEDMQEVVVVHKKRPVLDYQKHKAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480  
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DB 481 QMORLTNIITTEDIVTVVMTNVDPPKESL 513

RESULT 6

US-08-476-123-2  
; Sequence 2, Application US/08476123  
; Patent No. 6162896  
; GENERAL INFORMATION:  
; APPLICANT: Mathews, Lawrence S.  
; APPLICANT: Vale, Wylie W.  
; APPLICANT: Tsuchida, Kunihiro  
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF  
; TITLE OF INVENTION: RECEPTOR(S) OF THE ACTIVIN/TGF-BETA SUPERFAMILY  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/476,123  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/485,061  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/300,584  
; FILING DATE: 02-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/880,220  
; FILING DATE: 08-MAY-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/773,229

FILING DATE: 09-OCT-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/698,709  
FILING DATE: 10-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P41 9927  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 513 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-476-123-2

Query Match 99.7%; Score 2763; DB 4; Length 513;  
Best Local Similarity 99.4%; Pred. No. 6.2e-264;  
Matches 510; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MGAALKAFVFLISCGSAILGRSETQCLFFNANWEKDRNTQTVGPCYGDKDKRRHC 60
Db 1 MGAALKAFVFLISCGSAILGRSETQCLFFNANWEKDRNTQTVGPCYGDKDKRRHC 60
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Db 61 FATWKNISGSEIVKQGCWLDLINCYDRTDCIEKKDSPEVYFCCCGNMCNEKFSYPPEM 120
QY 121 EVTQTSNPVTPKPPYNNILYSLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDGP 180
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Db 301 AYLEDIPGLKDGHKPAISHRDIKSNVLLKNNLTACIADFGALKFEAGKSAGDTHGOV 360
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Db 421 QHPSLEDQVWVYHKKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCGVGERIT 480
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Db 481 QMORLNIITTEDIVTVMTNVDPPPKESSL 513
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RESULT 7  
US-08-738-1688-5  
Sequence 5, Application US/08738168B  
Patent No. 6132988  
GENERAL INFORMATION:  
APPLICANT: Sugino, Hiromu  
APPLICANT: Nakamura, Takanori  
APPLICANT: Shouji, Hiroki  
TITLE OF INVENTION: NEURONAL CELL-SPECIFIC RECEPTOR PROTEIN  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 Water Street

CITY: Boston  
STATE: MA USA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/738.168B  
FILING DATE: 25-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 280939/1995  
FILING DATE: 27-OCT-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 174909/1996  
FILING DATE: 04-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Resnick, David S.  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 342/46901  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 521 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-738-168B-5

Query Match 99.2%; Score 2749; DB 4; Length 521;  
Best Local Similarity 97.9%; Pred. No. 1.5e-262;  
Matches 510; Conservative 3; Mismatches 0; Indels 8; Gaps 1;

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QY 1 MGAALKAFVFLISCGSAILGRSETQCLFFNANWEKDRNTQTVGPCYGDKDKRRHC 60
Db 1 MGAALKAFVFLISCGSAILGRSETQCLFFNANWEKDRNTQTVGPCYGDKDKRRHC 60
QY 61 FATWKNISGSEIVKQGCWLDLINCYDRTDCVEKKDSPEVYFCCCGNMCNEKFSYPPEM 120
Db 61 FATWKNISGSEIVKQGCWLDLINCYDRTDCIEKKDSPEVYFCCCGNMCNEKFSYPPEM 120
QY 121 EVTQTSNPVTPKPPYNNILYSLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDGP 176
Db 121 EVTQTSNPVTPKPPYNNILYSLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDGP 180
QY 177 ----DPGPPPPSPLGLKPLQLLEVKARGCGVWKQALLNEYYAVKFIPIQDKQSWQNE 232
Db 177 ----DPGPPPPSPLGLKPLQLLEVKARGCGVWKQALLNEYYAVKFIPIQDKQSWQNE 240
QY 233 YEVYSLPQMKHENILQFIAEKGRTSVDVLDLWLTAFHEKGSLSDFLKNVLSNQLCHI 292
Db 233 YEVYSLPQMKHENILQFIAEKGRTSVDVLDLWLTAFHEKGSLSDFLKNVLSNQLCHI 300
QY 293 AETMARGLAYLHEDIPGLKDGHKPAISHRDIKSNVLLKNNLTACIADFGALKFEAGKS 352
Db 293 AETMARGLAYLHEDIPGLKDGHKPAISHRDIKSNVLLKNNLTACIADFGALKFEAGKS 360
QY 353 AGDTHGOVTRRYMAPEVEGAIFNFORDAFLRIDMYAMGLVWLWELASRCTAADGPVDEYM 412
Db 353 AGDTHGOVTRRYMAPEVEGAIFNFORDAFLRIDMYAMGLVWLWELASRCTAADGPVDEYM 420
QY 413 LPFEEIIGQHPSELDQVWVYHKKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSA 472
Db 413 LPFEEIIGQHPSELDQVWVYHKKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSA 480
QY 473 GCVCERITQMORLNIITTEDIVTVMTNVDPPPKESSL 513
Db 473 GCVCERITQMORLNIITTEDIVTVMTNVDPPPKESSL 521
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Tue May 13 17:51:40 2003

RESULT 8  
US-08-738-168B-15  
; Sequence 15 Application US/08738168B  
; Patent No. 6132988  
; GENERAL INFORMATION:  
; APPLICANT: Sugino, Hiromu  
; APPLICANT: Nakamura, Takanori  
; APPLICANT: Shouji, Hiroki  
; TITLE OF INVENTION: NEURONAL CELL-SPECIFIC RECEPTOR PROTEIN  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/738,168B  
; FILING DATE: 25-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 280939/1995  
; FILING DATE: 27-OCT-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 174909/1996  
; FILING DATE: 04-JUL-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Resnick, David S.  
; REGISTRATION NUMBER: 34,235  
; REFERENCE/DOCKET NUMBER: 342/46901  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 514 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-738-168B-15

Query Match 89.6%; Score 2482.5; DB 4; Length 514;  
Best Local Similarity 87.7%; Pred. No. 2.9e-236;  
Matches 451; Conservative 37; Mismatches 25; Indels 1; Gaps 1;  
  
Db 1 MGAALKAFVFLISCSGSGAILGRSETQCLFFNFANWEDRTNQTGVEPCYGDKRRH 59  
1 MGAATKLAFAVFLISCSGSGAILGRSETQCLFFNFANWEDRTNQTGVEPCYGDKRRH 60  
  
Qy 60 CFATWKNISGSIIEIVKQCWLDLINCVDRTDCVEKKDSEPEYVCCCGNMCNEKFSYFE 119  
61 CFATWKNISGSIIEIVKQCWLDLINCYNKSKCTEKKDSEPEYVCCCGNMCNEKFSYFE 120  
  
Db 120 MEVTOPTSNPTPKPPYNNILYSVLPLMLIAGIVICAFWYHHRMAYPPVLVPTQDPG 179  
121 MEVTOPTSNPTPKPPYNNILYSVLPLMLIAGIVICAFWYHHRMAYPPVLVPTQDPG 180  
  
Qy 180 PPPPSPLGLKPLQLLEVKARGCGVWKAQLLNEYAVKIFPIQDKQSQWNEYEYSLP 239  
181 PPPPSPLGLKPLQLLEVKARGCGVWKAQLLNEYAVKIFPIQDKQSQWNEYEYSLP 240  
  
Qy 240 GKNHENILQFTGAERGTSDVDLWLTAFHEKGSLSDFLKANYVSNOLCHIAETWARG 299  
241 GKNHENILQFTGAERGTSDVDLWLTAFHEKGSLSDFLKANYVSNOLCHIAETWARG 300  
  
Qy 300 LAYLHEDIPGLKDGHPAISHRDIKSKNVLKNNLTACIADFGALAKFEAGKSAGDTHGQ 359  
1 LAYLHEDIPGLKDGHPAISHRDIKSKNVLKNNLTACIADFGALAKFEAGKSAGDTHGQ 360

Db 301 LSHLHEDIPGLKDGHPAISHRDIKSKNVLKNNLTACIADFGALAKFEAGKSAGDTHGQ 360  
  
Qy 360 VGTTRYMAPEVLEGAINFQDAFLRIDMYAGLVWLWELASRCTAAGDPVDEYMLPFEEI 419  
361 VGTTRYMAPEVLEGAINFQDAFLRIDMYAGLVWLWELASRCTAAGDPVDEYMLPFEEI 420  
  
Qy 420 GQHSLEDMDQEVVYHKKRPVLYROYWQKHAGMAMLCETIEECWDHDAEARLSAGCVGERI 479  
421 GQHSLEDMDQEVVYHKKRPVLYROYWQKHAGMAMLCETIEECWDHDAEARLSAGCVGERI 480  
  
Qy 480 TOMQRLTNIITTEDIVTV 513  
481 TOMQRLTNIITTEDIVTV 514  
  
RESULT 9  
US-08-300-584-4  
; Sequence 4, Application US/08300584  
; Patent No. 5885794  
; GENERAL INFORMATION:  
; APPLICANT: Mathews, Lawrence S.  
; APPLICANT: Vale, Wylie W.  
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF  
; TITLE OF INVENTION: RECEPTOR(S) OF THE ACTIVIN/TGF-BETA SUPERFAMILY  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/300,584  
; FILING DATE: 02-SEP-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/880,220  
; FILING DATE: 08-MAY-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/773,229  
; FILING DATE: 09-OCT-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/698,709  
; FILING DATE: 10-MAY-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reiter, Stephen E.  
; REGISTRATION NUMBER: 31,192  
; REFERENCE/DOCKET NUMBER: P41 9806  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-546-9392  
; TELEFAX: 619-546-9392  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 510 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-300-584-4

Query Match 71.2%; Score 1971.5; DB 2; Length 510;  
Best Local Similarity 67.9%; Pred. No. 7.1e-186;  
Matches 349; Conservative 85; Mismatches 75; Indels 5; Gaps 3;  
  
Qy 1 MGAALKAFVFLISCSGSGAILGRSETQCLFFNFANWEDRTNQTGVEPCYGDKRRH 60  
1 MGAATKLAFAVFLISCSGSGAILGRSETQCLFFNFANWEDRTNQTGVEPCYGDKRRH 60  
  
Db 1 MGASVALTFLLLATFRAGSHDEVTRECIYNNANWELEKTNQSGVSECEGDKRLHC 60

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QY 61 FATWKNISGSIIEIVKQGCWLLDDINCVDKVEKSDPEVYFCCCEGNCMEKESYFPEM 120
Db 61 YASWRNNSGFIELYKKGWLLDDFNCYDQECIAKEENPQVFFCCCEGNYCNKFFHLPEV 120
QY 121 EYVQTPSNVPTPKPPYNNILYSVLPLMIAIGIVICAFWYRHHKMAYPVLPVPTQDGP 180
Db 121 EYVQTPSNVPTPKPPYNNILYSVLPLMIAIGIVICAFWYRHHKMAYPVLPVPTQDGP 180
QY 181 PPSPLGLKPLQLELVKARGFCVWKAQNLNEYVAVKIPFIQDKQSWQNEVEYSLPG 240
Db 181 PPSPLGLKPLQLELVKARGFCVWKAQNLNEYVAVKIPFIQDKQSWQNEVEYSLPG 240
QY 177 PPSPLGLKPLQLELVKARGFCVWKAQNLNEYVAVKIPFIQDKQSWQNEVEYSLPG 236
Db 177 PPSPLGLKPLQLELVKARGFCVWKAQNLNEYVAVKIPFIQDKQSWQNEVEYSLPG 236
QY 241 MKHENILOFIGAERKGTSDVDLWLTAFHEKGSLSDFLKANYVSNQOLCHIAETMARGL 300
Db 241 MKHENILOFIGAERKGTSDVDLWLTAFHEKGSLSDFLKANYVSNQOLCHIAETMARGL 300
QY 301 AYLEDIPGLK-DGHHKPAISHRDIKSNVLLKNNITACIADPGLAKFEAGKSAGDTHGQ 359
Db 301 AYLEDIPGLK-DGHHKPAISHRDIKSNVLLKNNITACIADPGLAKFEAGKSAGDTHGQ 359
QY 420 GQHSLEDQEVVHHKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCVGERI 479
Db 420 GQHSLEDQEVVHHKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCVGERI 479
QY 479 GQHSLEDQEVVHHKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCVGERI 479
Db 479 GQHSLEDQEVVHHKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCVGERI 479
QY 480 TOMORLNTIITTEDIVVTWTVNVDLPPKESSL 513
Db 480 TOMORLNTIITTEDIVVTWTVNVDLPPKESSL 513
QY 477 SOIRKSVNGTSDCLVSIIVTSVTVNVDLPPKESSI 510
Db 477 SOIRKSVNGTSDCLVSIIVTSVTVNVDLPPKESSI 510
RESULT 10
US-08-476-123-4
; Sequence 4, Application US/08476123
; Patent No. 6162896
; GENERAL INFORMATION:
; APPLICANT: Mathews, Lawrence S.
; APPLICANT: Vale, Willie W.
; APPLICANT: Tsuchida, Kunihiko
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
; TITLE OF INVENTION: RECEPTOR(S) OF THE ACTIVIN/TGF-BETA SUPERFAMILY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/485,061
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/300,584
; FILING DATE: 02-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/860,220
; FILING DATE: 08-MAY-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/773,229
; FILING DATE: 09-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/698,709
```

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; FILING DATE: 10-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9927
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 510 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-476-123-4
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Query Match 71.2%; Score 1971.5; DB 4; Length 510;
Best Local Similarity 67.9%; Pred. No. 7.1e-186;
Matches 349; Conservative 85; Mismatches 75; Indels 5; Gaps 3;
QY 1 MGAATAKLAFAVFLISGSGAILGRSETQCLFFNANWEKDRNTQGTGVPYCGDKRRHC 60
Db 1 MGAASVALTELLLATFRAGSGHDEVETRECIYINANWELEKTNQSGVESCEGEKDLRHC 60
QY 61 FATWKNISGSIIEIVKQGCWLLDDINCVDKVEKSDPEVYFCCCEGNCMEKESYFPEM 120
Db 61 YASWRNNSGFIELYKKGWLLDDFNCYDQECIAKEENPQVFFCCCEGNYCNKFFHLPEV 120
QY 121 EYVQTPSNVPTPKPPYNNILYSVLPLMIAIGIVICAFWYRHHKMAYPVLPVPTQDGP 180
Db 121 EYVQTPSNVPTPKPPYNNILYSVLPLMIAIGIVICAFWYRHHKMAYPVLPVPTQDGP 180
QY 181 PPSPLGLKPLQLELVKARGFCVWKAQNLNEYVAVKIPFIQDKQSWQNEVEYSLPG 240
Db 181 PPSPLGLKPLQLELVKARGFCVWKAQNLNEYVAVKIPFIQDKQSWQNEVEYSLPG 240
QY 177 PPSPLGLKPLQLELVKARGFCVWKAQNLNEYVAVKIPFIQDKQSWQNEVEYSLPG 236
Db 177 PPSPLGLKPLQLELVKARGFCVWKAQNLNEYVAVKIPFIQDKQSWQNEVEYSLPG 236
QY 241 MKHENILOFIGAERKGTSDVDLWLTAFHEKGSLSDFLKANYVSNQOLCHIAETMARGL 300
Db 241 MKHENILOFIGAERKGTSDVDLWLTAFHEKGSLSDFLKANYVSNQOLCHIAETMARGL 300
QY 301 AYLEDIPGLK-DGHHKPAISHRDIKSNVLLKNNITACIADPGLAKFEAGKSAGDTHGQ 359
Db 301 AYLEDIPGLK-DGHHKPAISHRDIKSNVLLKNNITACIADPGLAKFEAGKSAGDTHGQ 359
QY 420 GQHSLEDQEVVHHKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCVGERI 479
Db 420 GQHSLEDQEVVHHKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCVGERI 479
QY 479 GQHSLEDQEVVHHKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCVGERI 479
Db 479 GQHSLEDQEVVHHKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCVGERI 479
QY 480 TOMORLNTIITTEDIVVTWTVNVDLPPKESSL 513
Db 480 TOMORLNTIITTEDIVVTWTVNVDLPPKESSL 513
QY 477 SOIRKSVNGTSDCLVSIIVTSVTVNVDLPPKESSI 510
Db 477 SOIRKSVNGTSDCLVSIIVTSVTVNVDLPPKESSI 510
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RESULT 11
US-08-357-533A-12
; Sequence 12, Application US/08357533A
; Patent No. 5831050
; GENERAL INFORMATION:
; APPLICANT: JIN, DONALD F
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: KOBERSAMPATH, THANGAVEL
; APPLICANT: SMART, JOHN E
; TITLE OF INVENTION: NOVEL MORPHOGEN CELL SURFACE RECEPTOR
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,
; ADDRESSEE: INC
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
```

STATE: MA  
COUNTRY: USA  
ZIP: 01748  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/357,533A  
FILING DATE: 16-DEC-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: KELLY, ROBIN D  
REGISTRATION NUMBER: 34,637  
REFERENCE/DOCKET NUMBER: CRP-073FW  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (508)-435-9001  
TELEFAX: (508)-435-0992  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 536 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: protein  
LOCATION: 1..536  
OTHER INFORMATION: /note= "HUMAN ACTIVIN TYPE II  
OTHER INFORMATION: RECEPTOR"  
US-08-357-533A-12

Query Match 69.7%; Score 1931; DB 2; Length 536;  
Best Local Similarity 64.7%; Pred. No. 7.5e-182;  
Matches 343; Conservative 86; Mismatches 77; Indels 24; Gaps 2;  
QY 8 AFVFLISCSGAILGRSETQECLEFFNANWEKDRNTQGTVEPCYGDKKRRHCFATWNI 67  
DB 7 ALALLWGLSCLAGSGRGEAETRECIYYNANWELETRNOSGLERCEGEQDKRLHCYASWANS 66  
QY 68 SGSEIVKGCWGLDDINCYDRTDCVEKKDSPEYVFCCEGNCNEKFSYFPEMEVTOPTS 127  
DB 67 SGTEILVKKGCWGLDDINCYDQECVATEENPQVYFCCCEGNCNEKFSYFPEMEVTOPTS 126  
QY 128 NPVTPEKPPYNNILYSLVPLMLIAGIVICAFWYRHHKMAYPVPLV----- 173  
DB 127 EPPPTAPTLTLLVLAISLLPGLSLVLLAFWYRHHKPPYGHVDIHEVRQCORWAGRRD 186  
QY 174 -----PTQDPGPPPPSPPLGLKPLQLLEVKARGFCGWKAQLLNEYVAVKIFPIQ 224  
DB 187 GCADSEKPLPFQDPGPPPPSPPLVGLKPLQLLEIKARGFCGWKAQLMNDFAVAVKIFPLQ 246  
QY 225 DQSQNQEYEVYSLPGMKHENLQFVIGAEKRGTSVDVLDLITAFHEKGSLSDFLKANV 284  
DB 247 DQSQNQEYEVYSLPGMKHENLQFVIGAEKRGTSVDVLDLITAFHEKGSLSDFLKANV 306  
QY 285 SNNQLCHIAETMARGLAYLHEDIPGLK-DGHKPAISHRDIKSKNVLKNNLTACIADFLG 343  
DB 307 TWNELCHVAETMSRGLSYLHEDVPCWCEGEGHGPSIAHRDPKSKNVLKNSDLTAVLADFLG 366  
QY 344 ALKFAGKAGSAGTHQGVQVTRRYMAPEVLEGAINFQROAFRLIDMYAGLVLLWELASRCTA 403  
DB 367 AVRFEPGKPPGTHQGVQVTRRYMAPEVLEGAINFQROAFRLIDMYAGLVLLWELASRCTA 426  
QY 404 ADGPVDEYMLPPEEIGHPSELEDMQEVVVVHKKRPVLRDYWKHAGMAMLCETIERCWD 463  
DB 427 ADGPVDEYMLPPEEIGHPSELEDMQEVVVVHKKRPVLRDYWKHAGMAMLCETIERCWD 486  
QY 464 HDAEARLSAGCGERITOMQRLNITITTEDIVVTWVNTVDFPPKRESSL 513  
DB 487 HDAEARLSAGCGERITOMQRLNITITTEDIVVTWVNTVDFPPKRESSL 536

RESULT 12  
US-08-459-009-12  
Sequence 12, Application us/08459009  
Patent No. 5861479  
GENERAL INFORMATION:  
APPLICANT: JIN, DONALD F  
APPLICANT: OPPERMAN, HERMANN  
APPLICANT: KUBERASAMPATH, THANGAVEL  
APPLICANT: SMART, JOHN E  
TITLE OF INVENTION: NOVEL MORPHOGEN CELL SURFACE RECEPTOR  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,  
ADDRESS: INC  
STREET: 45 SOUTH STREET  
CITY: HOPKINTON  
STATE: MA  
COUNTRY: USA  
ZIP: 01748  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,009  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/357,533  
FILING DATE: 16-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: KELLY, ROBIN D  
REGISTRATION NUMBER: 34,637  
REFERENCE/DOCKET NUMBER: CRP-073FW  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (508)-435-9001  
TELEFAX: (508)-435-0992  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 536 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: protein  
LOCATION: 1..536  
OTHER INFORMATION: /note= "HUMAN ACTIVIN TYPE II  
OTHER INFORMATION: RECEPTOR"  
US-08-459-009-12

Query Match 69.7%; Score 1931; DB 2; Length 536;  
Best Local Similarity 64.7%; Pred. No. 7.5e-182;  
Matches 343; Conservative 86; Mismatches 77; Indels 24; Gaps 2;  
QY 8 AFVFLISCSGAILGRSETQECLEFFNANWEKDRNTQGTVEPCYGDKKRRHCFATWNI 67  
DB 7 ALALLWGLSCLAGSGRGEAETRECIYYNANWELETRNOSGLERCEGEQDKRLHCYASWANS 66  
QY 68 SGSEIVKGCWGLDDINCYDRTDCVEKKDSPEYVFCCEGNCNEKFSYFPEMEVTOPTS 127  
DB 67 SGTEILVKKGCWGLDDINCYDQECVATEENPQVYFCCCEGNCNEKFSYFPEMEVTOPTS 126  
QY 128 NPVTPEKPPYNNILYSLVPLMLIAGIVICAFWYRHHKMAYPVPLV----- 173  
DB 127 EPPPTAPTLTLLVLAISLLPGLSLVLLAFWYRHHKPPYGHVDIHEVRQCORWAGRRD 186  
QY 174 -----PTQDPGPPPPSPPLGLKPLQLLEVKARGFCGWKAQLLNEYVAVKIFPIQ 224  
DB 187 GCADSEKPLPFQDPGPPPPSPPLVGLKPLQLLEIKARGFCGWKAQLMNDFAVAVKIFPLQ 246

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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/357,533
FILING DATE: 16-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: KELLY, ROBIN D
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CRP-073FW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)-435-9001
TELEFAX: (508)-435-0992
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..536
OTHER INFORMATION: /note= "HUMAN ACTIVIN TYPE II
OTHER INFORMATION: RECEPTOR"
US-08-459-951-12

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## TELECOMMUNICATION INFORMATION:

TELEPHONE: (508)-435-9001

TELEFAX: (508)-435-0992

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 513 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Protein

LOCATION: 1..513

OTHER INFORMATION: /note= "RAT ACTIVIN TYPE II

RECEPTOR"

US-08-357-533A-11

Query Match 69.2%; Score 1915.5; DB 2; Length 513;  
Best Local Similarity 67.1%; Pred. No. 2.4e-180;  
Matches 341; Conservative 85; Mismatches 79; Indels 3; Gaps 3;

QY 8 AFAPVLISCSGAILGRSETQECLEFFANWKEKDRNTQTVGECYGDKDKRRHCFATWKNI 67

7 ALALLWSLCSAGSGRGEARETCIYYANWLELRTNSGLERCEGEQDKRLHCYASWPNS 66

68 SGSEIVKQGCWLDIDNCYDRDTCVEKKDSPEYVFCCEGNCMCNEKFSYPPEMEVTOPTS 127

67 SGTIELVKKGCWLDIDNCYDRDTCVEKKDSPEYVFCCEGNCMCNEKFSYPPEMEVTOPTS 126

128 NPVTTPKPPYNNILYSLVPLMILAGIVICAFWVYRHHKMAYPVLPVTDGPPPPSPLL 187

127 EPPPTAPTLTTLVLAISLLPIGGLSLVLLAFWYRHHKMAYPVLPVTDGPPPPSPLL 185

188 GLKPLQLLEVKARGFCGCVKWAQILNEXVAVKIFPIQDKQSWQNEVEYVSLPGMKHENIL 247

186 GLKPLQLLEVKARGFCGCVKWAQILNEXVAVKIFPIQDKQSWQNEVEYVSLPGMKHENIL 245

248 QFIAEKKRGTS-VVDVLMLITAFHEKGSLSDFLKANVSVNQLCHIAETMARGLAYLHED 306

246 QFIAEKKRGTS-VVDVLMLITAFHEKGSLSDFLKANVSVNQLCHIAETMARGLAYLHED 305

307 IPGLK-DGKHKAISHRDIKSKNVLKNNLTACIADFLGALKFEAGKSAGDTHGOVGTTRY 365

306 VPMCRGEGHKPSIAHRDIFKSNVLKNNLTACIADFLGALKFEAGKSAGDTHGOVGTTRY 365

366 MAPEVLEGAINFORDAFRLIDMYAMGLVWELASRCATADGPVDEYMLPFEIEIGQHPSL 425

366 MAPEVLEGAINFORDAFRLIDMYAMGLVWELASRCATADGPVDEYMLPFEIEIGQHPSL 425

426 EDMQEVVYVHKRRPVLRYDQWOKHAGMAMLCETIEECWDHDAEARLSAGCVGERITQMORL 485

426 EELQEVVYVHKRRPVLRYDQWOKHAGMAMLCETIEECWDHDAEARLSAGCVGERITQMORL 485

486 TWIITTEDIVVTMTVNVDPKPSL 513

486 VNGSTDCSLVSLVSTNVDPKPSL 513

## RESULT 15

US-08-459-009-11

Sequence 11, Application US/08459009

Patent No. 5861479

GENERAL INFORMATION:

APPLICANT: JIN, DONALD F

APPLICANT: OPPERMANN, HERMANN

APPLICANT: KUBERASAMPATH, THANGAVEL

APPLICANT: SMART, JOHN E

TITLE OF INVENTION: NOVEL MORPHOGEN CELL SURFACE RECEPTOR

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,

ADDRESSEE: INC

STREET: 45 SOUTH STREET

CITY: HOPKINTON

STATE: MA

COUNTRY: USA

ZIP: 01748

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,009

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/357,533

FILING DATE: 16-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: KELLY, ROBIN D

REGISTRATION NUMBER: 34,637

REFERENCE/DOCKET NUMBER: CRP-073FW

TELECOMMUNICATION INFORMATION:

TELEPHONE: (508)-435-9001

TELEFAX: (508)-435-0992

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 513 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Protein

LOCATION: 1..513

OTHER INFORMATION: /note= "RAT ACTIVIN TYPE II

RECEPTOR"

US-08-459-009-11

Query Match 69.2%; Score 1915.5; DB 2; Length 513;  
Best Local Similarity 67.1%; Pred. No. 2.4e-180;  
Matches 341; Conservative 85; Mismatches 79; Indels 3; Gaps 3;

QY 8 AFAPVLISCSGAILGRSETQECLEFFANWKEKDRNTQTVGECYGDKDKRRHCFATWKNI 67

7 ALALLWSLCSAGSGRGEARETCIYYANWLELRTNSGLERCEGEQDKRLHCYASWPNS 66

68 SGSEIVKQGCWLDIDNCYDRDTCVEKKDSPEYVFCCEGNCMCNEKFSYPPEMEVTOPTS 127

67 SGTIELVKKGCWLDIDNCYDRDTCVEKKDSPEYVFCCEGNCMCNEKFSYPPEMEVTOPTS 126

128 NPVTTPKPPYNNILYSLVPLMILAGIVICAFWVYRHHKMAYPVLPVTDGPPPPSPLL 187

127 EPPPTAPTLTTLVLAISLLPIGGLSLVLLAFWYRHHKMAYPVLPVTDGPPPPSPLL 185

188 GLKPLQLLEVKARGFCGCVKWAQILNEXVAVKIFPIQDKQSWQNEVEYVSLPGMKHENIL 247

186 GLKPLQLLEVKARGFCGCVKWAQILNEXVAVKIFPIQDKQSWQNEVEYVSLPGMKHENIL 245

248 QFIAEKKRGTS-VVDVLMLITAFHEKGSLSDFLKANVSVNQLCHIAETMARGLAYLHED 306

246 QFIAEKKRGTS-VVDVLMLITAFHEKGSLSDFLKANVSVNQLCHIAETMARGLAYLHED 305

307 IPGLK-DGKHKAISHRDIKSKNVLKNNLTACIADFLGALKFEAGKSAGDTHGOVGTTRY 365

306 VPMCRGEGHKPSIAHRDIFKSNVLKNNLTACIADFLGALKFEAGKSAGDTHGOVGTTRY 365

366 MAPEVLEGAINFORDAFRLIDMYAMGLVWELASRCATADGPVDEYMLPFEIEIGQHPSL 425

366 MAPEVLEGAINFORDAFRLIDMYAMGLVWELASRCATADGPVDEYMLPFEIEIGQHPSL 425

426 EDMQEVVYVHKRRPVLRYDQWOKHAGMAMLCETIEECWDHDAEARLSAGCVGERITQMORL 485

426 EELQEVVYVHKRRPVLRYDQWOKHAGMAMLCETIEECWDHDAEARLSAGCVGERITQMORL 485



us-09-742-684a-16.rai

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QY      486   T N I I T T E D I V T V M V T N V D F P P K E S S L    513  
          | _ :: :|::|| |||||  
Db      486   V N G S T D C L V S L V T S S T N V D L L P K E S S I    513
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Search completed: May 10, 2003, 18:00:34  
Job time : 18 secs



GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2003, 17:55:10 ; Search time 21 Seconds  
(without alignments)  
2348.427 Million cell updates/sec

Title: US-09-742-684A-16  
Perfect score: 2770  
Sequence: 1 MGAALAFVAVELISCSGA.....IVTVVTMTNVDFPPRESSL 513

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR-73:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | ID     | Description        |
|------------|--------|-------------|--------|--------|--------------------|
| 1          | 2767   | 99.9        | 513    | JQ1486 | activin receptor I |
| 2          | 2763   | 99.7        | 513    | A39896 | activin receptor p |
| 3          | 2762   | 99.7        | 513    | S27258 | activin receptor t |
| 4          | 2759   | 99.6        | 513    | A49193 | type II activin re |
| 5          | 2743   | 99.0        | 513    | I45850 | activin receptor t |
| 6          | 2604   | 94.0        | 513    | S23089 | activin receptor t |
| 7          | 2482.5 | 89.6        | 514    | JQ1317 | activin receptor p |
| 8          | 2474.5 | 89.3        | 512    | S21171 | activin receptor S |
| 9          | 1971.5 | 71.2        | 510    | A42635 | activin receptor S |
| 10         | 1965.5 | 71.0        | 510    | A56926 | activin receptor I |
| 11         | 1940   | 70.0        | 512    | I37134 | activin type II re |
| 12         | 1935   | 69.9        | 512    | D40829 | activin receptor i |
| 13         | 1934   | 69.8        | 536    | A40829 | activin receptor i |
| 14         | 1923   | 69.4        | 504    | B40829 | activin receptor i |
| 15         | 1922   | 69.4        | 528    | D40829 | activin receptor i |
| 16         | 1915.5 | 69.2        | 513    | JQ1484 | activin receptor p |
| 17         | 1472   | 53.1        | 382    | B49193 | type II activin re |
| 18         | 1312.5 | 47.4        | 365    | S27268 | activin receptor S |
| 19         | 1147.5 | 41.4        | 356    | A48678 | activin receptor I |
| 20         | 1051   | 37.9        | 251    | PC2461 | activin type II re |
| 21         | 975    | 35.2        | 175    | I57667 | activin receptor - |
| 22         | 789.5  | 28.5        | 557    | I50429 | transforming growt |
| 23         | 779    | 28.1        | 592    | S51371 | transforming growt |
| 24         | 777.5  | 28.1        | 567    | JN0459 | transforming growt |
| 25         | 775.5  | 28.0        | 592    | A42100 | transforming growt |
| 26         | 775.5  | 28.0        | 1038   | I38935 | bone morphogenetic |
| 27         | 774.5  | 28.0        | 567    | A44225 | transforming growt |
| 28         | 770.5  | 27.8        | 1038   | JC5527 | bone morphogenetic |
| 29         | 763.5  | 27.6        | 478    | JC5373 | transforming growt |

|    |       |      |     |   |        |                    |
|----|-------|------|-----|---|--------|--------------------|
| 30 | 674   | 24.3 | 532 | 2 | I37163 | ALK-3 - human      |
| 31 | 669   | 24.2 | 532 | 2 | A56238 | bone morphogenetic |
| 32 | 664   | 24.0 | 532 | 2 | JC2387 | bone morphogenetic |
| 33 | 662.5 | 23.9 | 527 | 2 | A54985 | BMP receptor precu |
| 34 | 653.5 | 23.6 | 502 | 2 | JC2491 | serine/threonine k |
| 35 | 647.5 | 23.4 | 502 | 2 | A53444 | activin receptor-l |
| 36 | 634.5 | 22.9 | 440 | 2 | A56693 | receptor protein k |
| 37 | 634.5 | 22.9 | 601 | 2 | A59921 | serine/threonine k |
| 38 | 624.5 | 22.5 | 502 | 2 | A56683 | receptor protein k |
| 39 | 624   | 22.5 | 503 | 2 | A49432 | activin receptor-l |
| 40 | 622.5 | 22.5 | 503 | 2 | JC2061 | transforming growt |
| 41 | 621.5 | 22.4 | 499 | 2 | JC2062 | transforming growt |
| 42 | 613.5 | 22.1 | 505 | 2 | I38859 | activin A receptor |
| 43 | 611.5 | 22.1 | 505 | 2 | I53417 | type I serine-thre |
| 44 | 587.5 | 21.2 | 509 | 2 | A45992 | activin A receptor |
| 45 | 587   | 21.2 | 509 | 2 | I45713 | Dpp receptor TKV,  |

ALIGNMENTS

RESULT 1  
JQ1486  
activin receptor II precursor - human  
N:Contains: serine/threonine-specific protein kinase (EC 2.7.1.1.-)  
C:Species: Homo sapiens (man)  
C>Date: 17-Jul-1992 #sequence\_revision 19-Oct-1995 #text\_change 21-Jul-2000  
C:Accession: JQ1486; S18908; S22345  
R:Donaldson, C.J.; Mathews, L.S.; Vale, W.W.  
Biochem. Biophys. Res. Commun. 184, 310-316, 1992  
A:Title: Molecular cloning and binding properties of the human type II activin recept  
A:Reference number: JQ1486; MUID:92231944; PMID:13114589  
A:Accession: JQ1486  
A:Molecule type: mRNA  
A:Residues: 1-513 <DON>  
A:Cross-references: GB:M93415; NID:g178049; PIDN:AAA35504.1; PID:g178050  
A:Experimental source: testis  
R:Geisler, A.G.  
submitted to the EMBL Data Library, December 1991  
A:Reference number: S18908  
A:Accession: S18908  
A:Molecule type: mRNA  
A:Residues: 1-513 <GEI>  
A:Cross-references: EMBL:X62381; NID:g28347; PIDN:CAA44245.1; PID:g28348  
A:Experimental source: mammary gland epithelial cell line B5-589  
R:Matzuk, M.M.; Bradley, A.  
Biochim. Biophys. Acta 1130, 105-108, 1992  
A:Title: Cloning of the human activin receptor cDNA reveals high evolutionary conserv  
A:Reference number: S22345; MUID:92182002; PMID:1311955  
A:Accession: S22345  
A:Molecule type: mRNA  
A:Residues: 1-513 <MAT2>  
A:Cross-references: EMBL:X63128; NID:g3928172; PIDN:CAA44839.1; PID:g28350  
C:Comment: This protein binds activin A.  
C:Genetics:  
A:Gene: GDB:ACVR2  
A:Cross-references: GDB:I32411  
A:Map position: liqj3-liqj3  
C:Superfamily: activin receptor II; protein kinase homology  
C:Keywords: ATP; glycoprotein; phosphotransferase; receptor; serine/threonine-specifi  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-513/Product: activin receptor II #status predicted <EXT>  
F:20-138/Domain: extracellular #status predicted <MAT>  
F:139-160/Domain: transmembrane #status predicted <INT>  
F:161-513/Domain: intracellular #status predicted <INT>  
F:190-486/Domain: protein kinase homology <SKIN>  
F:199-206/Region: protein kinase ATP-binding motif  
F:43,66/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:219/Active site: Lys #status predicted

Query Match 99.9%; Score 2767; DB 1; Length 513;  
Best Local Similarity 99.8%; Pred. No. 9.4e-142;  
Matches 512; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAALKAFVFLISCGSAILGRSETQECLEFFNANWEKDRNTQGTGVEPCYGDKRRHC 60  
 Db 1 MGAALKAFVFLISCGSAILGRSETQECLEFFNANWEKDRNTQGTGVEPCYGDKRRHC 60  
 QY 61 FATWKNISGSIEIVKQGCWLDINCVDRTDCVEKKDSPEVYFCCCEGNCNEKFSYFPEM 120  
 Db 61 FATWKNISGSIEIVKQGCWLDINCVDRTDCVEKKDSPEVYFCCCEGNCNEKFSYFPEM 120  
 QY 121 EVTQPTSNPTPKPPYYNLLYSVPLMLTAGIVICAFWYRHHKMAYPVLPVPTQDGP 180  
 Db 121 EVTQPTSNPTPKPPYYNLLYSVPLMLTAGIVICAFWYRHHKMAYPVLPVPTQDGP 180  
 QY 181 PPPSPLLGLKPLQLLEVKGARFGCVKKAQLLNEYVAVKIFPIQDKSQWNEYEYVSLPG 240  
 Db 181 PPPSPLLGLKPLQLLEVKGARFGCVKKAQLLNEYVAVKIFPIQDKSQWNEYEYVSLPG 240  
 QY 241 MKENILQFIGAERKGTSDVDLMLITAFHEKGSLSDFLKANVYSWNLCHIAETMARGL 300  
 Db 241 MKENILQFIGAERKGTSDVDLMLITAFHEKGSLSDFLKANVYSWNLCHIAETMARGL 300  
 QY 301 AYLEDIPGLKDGHPKPAISHRDIKSKNVLKNNLTACIADFGALKFEAGKSAGDTHGQV 360  
 Db 301 AYLEDIPGLKDGHPKPAISHRDIKSKNVLKNNLTACIADFGALKFEAGKSAGDTHGQV 360  
 QY 361 GTRRYMAPEVLEGAINFORDAFLRDMYAMGLVWLWELASRCTAADGPDVDEYMLPFEIEIG 420  
 Db 361 GTRRYMAPEVLEGAINFORDAFLRDMYAMGLVWLWELASRCTAADGPDVDEYMLPFEIEIG 420  
 QY 421 QHPSEDMQEVVVHKKRPVLDYQWKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480  
 Db 421 QHPSEDMQEVVVHKKRPVLDYQWKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480  
 QY 481 QMORLTNIITTEDIVVTMTNVDPPKESL 513  
 Db 481 QMORLTNIITTEDIVVTMTNVDPPKESL 513

## RESULT 2

A39896  
 activin receptor precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 18-Jun-1999  
 C:Accession: A39896  
 R:Mathews, L.S.; Vale, W.W.  
 Cell 65, 973-982, 1991  
 A>Title: Expression cloning of an activin receptor, a predicted transmembrane protein  
 A:Reference number: A39896; MUID:91256317; PMID:1646080  
 A:Accession: A39896  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-513 <MAT>  
 A:Cross-references: GB:M65287; NID:g191663; PIDN:AAA3171.1; PID:g191664  
 C:Superfamily: activin receptor II; protein kinase homology  
 C:Keywords: ATP; receptor; serine/threonine-specific protein kinase; transmembrane protein  
 F:190-486/Domain: protein kinase homology <KIN>

Query Match 99.7%; Score 2763; DB 2; Length 513;  
 Best Local Similarity 99.4%; Pred. No. 1.5e-141;  
 Matches 510; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAALKAFVFLISCGSAILGRSETQECLEFFNANWEKDRNTQGTGVEPCYGDKRRHC 60  
 Db 1 MGAALKAFVFLISCGSAILGRSETQECLEFFNANWEKDRNTQGTGVEPCYGDKRRHC 60  
 QY 61 FATWKNISGSIEIVKQGCWLDINCVDRTDCVEKKDSPEVYFCCCEGNCNEKFSYFPEM 120  
 Db 61 FATWKNISGSIEIVKQGCWLDINCVDRTDCIEKKDSPEVYFCCCEGNCNEKFSYFPEM 120  
 QY 121 EVTQPTSNPTPKPPYYNLLYSVPLMLTAGIVICAFWYRHHKMAYPVLPVPTQDGP 180  
 Db 121 EVTQPTSNPTPKPPYYNLLYSVPLMLTAGIVICAFWYRHHKMAYPVLPVPTQDGP 180

QY 181 PPPSPLLGLKPLQLLEVKGARFGCVKKAQLLNEYVAVKIFPIQDKSQWNEYEYVSLPG 240  
 Db 181 PPPSPLLGLKPLQLLEVKGARFGCVKKAQLLNEYVAVKIFPIQDKSQWNEYEYVSLPG 240  
 QY 241 MKENILQFIGAERKGTSDVDLMLITAFHEKGSLSDFLKANVYSWNLCHIAETMARGL 300  
 Db 241 MKENILQFIGAERKGTSDVDLMLITAFHEKGSLSDFLKANVYSWNLCHIAETMARGL 300  
 QY 301 AYLEDIPGLKDGHPKPAISHRDIKSKNVLKNNLTACIADFGALKFEAGKSAGDTHGQV 360  
 Db 301 AYLEDIPGLKDGHPKPAISHRDIKSKNVLKNNLTACIADFGALKFEAGKSAGDTHGQV 360  
 QY 361 GTRRYMAPEVLEGAINFORDAFLRDMYAMGLVWLWELASRCTAADGPDVDEYMLPFEIEIG 420  
 Db 361 GTRRYMAPEVLEGAINFORDAFLRDMYAMGLVWLWELASRCTAADGPDVDEYMLPFEIEIG 420  
 QY 421 QHPSEDMQEVVVHKKRPVLDYQWKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480  
 Db 421 QHPSEDMQEVVVHKKRPVLDYQWKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480  
 QY 481 QMORLTNIITTEDIVVTMTNVDPPKESL 513  
 Db 481 QMORLTNIITTEDIVVTMTNVDPPKESL 513

## RESULT 3

S27258  
 activin receptor type II - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 18-Jun-1999  
 C:Accession: S27258  
 R:Shinozaki, H.; Ito, I.; Hasegawa, Y.; Nakamura, K.; Igarashi, S.; Nakamura, M.; Miy  
 FEBS Lett. 312, 53-56, 1992  
 A>Title: Cloning and sequencing of a rat type II activin receptor.  
 A:Reference number: S27258; MUID:93050162; PMID:1385212  
 A:Accession: S27258  
 A:Molecule type: mRNA  
 A:Residues: 1-513 <SHI>  
 A:Cross-references: GB:S48190; NID:g258941; PIDN:AAB23958.1; PID:g258942  
 C:Superfamily: activin receptor II; protein kinase homology  
 C:Keywords: ATP; receptor  
 F:190-486/Domain: protein kinase homology <KIN>

Query Match 99.7%; Score 2762; DB 2; Length 513;  
 Best Local Similarity 99.2%; Pred. No. 1.7e-141;  
 Matches 509; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAALKAFVFLISCGSAILGRSETQECLEFFNANWEKDRNTQGTGVEPCYGDKRRHC 60  
 Db 1 MGAALKAFVFLISCGSAILGRSETQECLEFFNANWEKDRNTQGTGVEPCYGDKRRHC 60  
 QY 61 FATWKNISGSIEIVKQGCWLDINCVDRTDCVEKKDSPEVYFCCCEGNCNEKFSYFPEM 120  
 Db 61 FATWKNISGSIEIVKQGCWLDINCVDRTDCIEKKDSPEVYFCCCEGNCNEKFSYFPEM 120  
 QY 121 EVTQPTSNPTPKPPYYNLLYSVPLMLTAGIVICAFWYRHHKMAYPVLPVPTQDGP 180  
 Db 121 EVTQPTSNPTPKPPYYNLLYSVPLMLTAGIVICAFWYRHHKMAYPVLPVPTQDGP 180  
 QY 181 PPPSPLLGLKPLQLLEVKGARFGCVKKAQLLNEYVAVKIFPIQDKSQWNEYEYVSLPG 240  
 Db 181 PPPSPLLGLKPLQLLEVKGARFGCVKKAQLLNEYVAVKIFPIQDKSQWNEYEYVSLPG 240  
 QY 241 MKENILQFIGAERKGTSDVDLMLITAFHEKGSLSDFLKANVYSWNLCHIAETMARGL 300  
 Db 241 MKENILQFIGAERKGTSDVDLMLITAFHEKGSLSDFLKANVYSWNLCHIAETMARGL 300  
 QY 301 AYLEDIPGLKDGHPKPAISHRDIKSKNVLKNNLTACIADFGALKFEAGKSAGDTHGQV 360  
 Db 301 AYLEDIPGLKDGHPKPAISHRDIKSKNVLKNNLTACIADFGALKFEAGKSAGDTHGQV 360  
 QY 361 GTRRYMAPEVLEGAINFORDAFLRDMYAMGLVWLWELASRCTAADGPDVDEYMLPFEIEIG 420

Db 361 GTRRYMAPEVLEGAINFQDAFLRIDMYAMGLVWLWELASRCTAAGDPVDEYMLPFEEIG 420  
QY 421 QHPSLEDMQEVVHHKKRPVLDYWKHAGNMLCETIEECWDHDAEARSAGCVGERIT 480  
Db 421 QHPSLEDMQEVVHHKKRPVLDYWKHAGNMLCETIEECWDHDAEARSAGCVGERIT 480  
QY 481 QMORLTNIITTEDIVVTVMVNTVNDPPPKSSSL 513  
Db 481 QMORLTNIITTEDIVVTVMVNTVNDPPPKSSSL 513

RESULT 4

A49193  
type II activin receptor ActRII - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-May-1997  
C:Accession: A49193  
R:Eng, Z.M.; Madigan, M.B.; Chen, C.L.  
Endocrinology 132, 2593-2600, 1993  
A:Title: Expression of type II activin receptor genes in the male and female reproductiv  
A:Reference number: A49193; MUID:93279247; PMID:7916681  
A:Accession: A49193  
A:Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-513 <FEN>  
A:Note: sequence extracted from NCBI backbone (NCBIN:133008, NCBI:133009)  
C:Superfamily: activin receptor II; protein kinase homology  
C:Keywords: ATP; receptor  
F:190-486/Domain: protein kinase homology <KIN>

Query Match 99.6%; Score 2759; DB 2; Length 513;  
Best Local Similarity 99.2%; Pred. No. 2.5e-141;  
Matches 509; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGAALKAFVFLISCGSAILGRSETQECLEFFNANWEKDRNTQGTVEPCYGDKKRRHC 60  
Db 1 MGAALKAFVFLISCGSAILGRSETQECLEFFNANWEKDRNTQGTVEPCYGDKKRRHC 60  
QY 61 FATWKNISGSIEIVKQGCWLDLDINCYDRTDCIEKKDSPEVYFCCCGNMCNEKFSYFPEM 120  
Db 61 FATWKNISGSIEIVKQGCWLDLDINCYDRTDCIEKKDSPEVYFCCCGNMCNEKFSYFPEM 120  
QY 121 EVTQPTSNPVPKPPYNNILLYSLVPLMLIAGIVICAFWYRHHKMAYPVPLVPTQDPGP 180  
Db 121 EVTQPTSNPVPKPPYNNILLYSLVPLMLIAGIVICAFWYRHHKMAYPVPLVPTQDPGP 180  
QY 181 PPPSLGLKPLQLLEVKARGFCVWKAQLNEYVAVKIFPIQDKQSWQNEYEYVSLPG 240  
Db 181 PPPSLGLKPLQLLEVKARGFCVWKAQLNEYVAVKIFPIQDKQSWQNEYEYVSLPG 240  
QY 241 MKHENILQFTGAERKGTSDVDLWLITAFHEKGSLSDFLKANYVSNWNLCHIAETMARGL 300  
Db 241 MKHENILQFTGAERKGTSDVDLWLITAFHEKGSLSDFLKANYVSNWNLCHIAETMARGL 300  
QY 301 AYLHEDIPGLKDGKHPAISHRDIKSNVLLKNNLTACIADFGALKFEAGKSAGDTHGOV 360  
Db 301 AYLHEDIPGLKDGKHPAISHRDIKSNVLLKNNLTACIADFGALKFEAGKSAGDTHGOV 360  
QY 361 GTRRYMAPEVLEGAINFQDAFLRIDMYAMGLVWLWELASRCTAAGDPVDEYMLPFEEIG 420  
Db 361 GTRRYMAPEVLEGAINFQDAFLRIDMYAMGLVWLWELASRCTAAGDPVDEYMLPFEEIG 420  
QY 421 QHPSLEDMQEVVHHKKRPVLDYWKHAGNMLCETIEECWDHDAEARSAGCVGERIT 480  
Db 421 QHPSLEDMQEVVHHKKRPVLDYWKHAGNMLCETIEECWDHDAEARSAGCVGERIT 480  
QY 481 QMORLTNIITTEDIVVTVMVNTVNDPPPKSSSL 513  
Db 481 QMORLTNIITTEDIVVTVMVNTVNDPPPKSSSL 513

RESULT 5

I45850

activin receptor type II - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 15-Oct-1996 #sequence\_revision 15-Oct-1996 #text\_change 18-Jun-1999  
C:Accession: I45850  
R:Ethier, J.F.; Houde, A.; Lussier, J.G.; Silversides, D.W.  
Mol. Cell. Endocrinol. 106, 1-8, 1994  
A:Title: Bovine activin receptor type II cDNA: cloning and tissue expression.  
A:Reference number: I45850; MUID:95203477; PMID:7534730  
A:Accession: I45850  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-513 <ETH>  
A:Cross-references: GB:L21717; NID:g393113; PIDN:AAA74597.1; PID:g393114  
C:Genetics:  
A:Gene: actRII  
C:Superfamily: activin receptor II; protein kinase homology  
C:Keywords: ATP; receptor  
F:190-486/Domain: protein kinase homology <KIN>

Query Match 99.0%; Score 2743; DB 2; Length 513;  
Best Local Similarity 98.4%; Pred. No. 1.8e-140;  
Matches 505; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGAALKAFVFLISCGSAILGRSETQECLEFFNANWEKDRNTQGTVEPCYGDKKRRHC 60  
Db 1 MGAALKAFVFLISCGSAILGRSETQECLEFFNANWEKDRNTQGTVEPCYGDKKRRHC 60  
QY 61 FATWKNISGSIEIVKQGCWLDLDINCYDRTDCIEKKDSPEVYFCCCGNMCNEKFSYFPEM 120  
Db 61 FATWKNISGSIEIVKQGCWLDLDINCYDRTDCIEKKDSPEVYFCCCGNMCNEKFSYFPEM 120  
QY 121 EVTQPTSNPVPKPPYNNILLYSLVPLMLIAGIVICAFWYRHHKMAYPVPLVPTQDPGP 180  
Db 121 EVTQPTSNPVPKPPYNNILLYSLVPLMLIAGIVICAFWYRHHKMAYPVPLVPTQDPGP 180  
QY 181 PPPSLGLKPLQLLEVKARGFCVWKAQLNEYVAVKIFPIQDKQSWQNEYEYVSLPG 240  
Db 181 PPPSLGLKPLQLLEVKARGFCVWKAQLNEYVAVKIFPIQDKQSWQNEYEYVSLPG 240  
QY 241 MKHENILQFTGAERKGTSDVDLWLITAFHEKGSLSDFLKANYVSNWNLCHIAETMARGL 300  
Db 241 MKHENILQFTGAERKGTSDVDLWLITAFHEKGSLSDFLKANYVSNWNLCHIAETMARGL 300  
QY 301 AYLHEDIPGLKDGKHPAISHRDIKSNVLLKNNLTACIADFGALKFEAGKSAGDTHGOV 360  
Db 301 AYLHEDIPGLKDGKHPAISHRDIKSNVLLKNNLTACIADFGALKFEAGKSAGDTHGOV 360  
QY 361 GTRRYMAPEVLEGAINFQDAFLRIDMYAMGLVWLWELASRCTAAGDPVDEYMLPFEEIG 420  
Db 361 GTRRYMAPEVLEGAINFQDAFLRIDMYAMGLVWLWELASRCTAAGDPVDEYMLPFEEIG 420  
QY 421 QHPSLEDMQEVVHHKKRPVLDYWKHAGNMLCETIEECWDHDAEARSAGCVGERIT 480  
Db 421 QHPSLEDMQEVVHHKKRPVLDYWKHAGNMLCETIEECWDHDAEARSAGCVGERIT 480  
QY 481 QMORLTNIITTEDIVVTVMVNTVNDPPPKSSSL 513  
Db 481 QMORLTNIITTEDIVVTVMVNTVNDPPPKSSSL 513

RESULT 6

S23089  
activin receptor type IIA - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Jun-2000  
C:Accession: S23089  
R:Ohuchi, H.; Noji, S.; Koyama, E.; Myokai, F.; Nishikawa, K.; Nohno, T.; Tashiro, K.  
FEBS Lett. 303, 185-189, 1992  
A:Title: Expression pattern of the activin receptor type IIA gene during differentiat  
A:Reference number: S23089; MUID:92299088; PMID:1318847  
A:Accession: S23089  
A:Status: preliminary  
A:Molecule type: mRNA

A:Residues: 1-513 <OHU>  
 A:Cross-references: GB:D31899; NID:g505347; PIDN:BAA06697.1; PID:g505348  
 C:Superfamily: activin receptor II; protein kinase homology  
 C:Keywords: ATP  
 F:190-486/Domain: protein kinase homology <KIN>

Query Match 94.0%; Score 2604; DB 2; Length 513;  
 Best Local Similarity 92.2%; Pred. No. 5.4e-133;  
 Matches 473; Conservative 26; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MGAARKLAFVFLISCSGAILGRSETQCLFFNANWEKDRNTQGTGVEPCYGDKRRHC 60  
 Db 1 MGAATLALAVFLISCSGAILGRSETQCIYYNANWEKDKTAVGTEPCYGDKRRHC 60  
 Qy 61 FATWKNISGSIEIVKQGWLDLDCYDRDTCVEKKDSPEYVFCCCGNMCNEKFSYFPEM 120  
 Db 61 FATWKNISGSIEIVKQGWLDLDCYDRDTCIEKKDSPEYVFCCCGNMCNEKFSYFPEM 120  
 Qy 121 EVTQPTSNVTPKPPYYNILLISLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDPGP 180  
 Db 121 EVTQPTSNVTPKPPYYNILLISLVPLIMGIAVIVLFSFWMYRHHKLAYPPVLPVPTQDPGP 180  
 Qy 181 PPPSPILGLPLQLLEVKARGFCGVKQAQLNEYVAVKIFPIQDKOSWQNEVEYISLPG 240  
 Db 181 PPPSPILGLPLQLLEVKARGFCGVKQAQLNEYVAVKIFPIQDKOSWQNEVEYISLPG 240  
 Qy 241 MKHNNILQFIAEGRGTSVDVLDLITAFHEKGSLSDFLKANYVSNQLCHIAETMARGL 300  
 Db 241 MKHNNILQFIAEGRGTSVDVLDLITAFHEKGSLSDFLKANYVSNNELCHIAETMARGL 300  
 Qy 301 AYLHEDIPGLKDGHPKPAISHRDIKSNVLLKNNLTACIADFGALALFEAGKSAGDTHGOV 360  
 Db 301 AYLHEDIPGLKDGHPKPAISHRDIKSNVLLKNNLTACIADFGALALFEAGKSAGDTHGOV 360  
 Qy 361 GTRRYMAPEVLEGAINFORDAFLRDMYAMGLVWLASRCTAAGDPVDEYMLPFEEIG 420  
 Db 361 GTRRYMAPEVLEGAINFORDAFLRDMYAMGLVWLASRCTAAGDPVDEYMLPFEEIG 420  
 Qy 421 QHPSLEDQEVVVHKKRPVLRDYQKQHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480  
 Db 421 QHPSLEDQEVVVHKKRPVLRDYQKQHAGMAMLCETIEECWDHDAEARLSAGCVGERII 480  
 Qy 481 QMORLTNIITTEDIVVTWTVNVDPPPKESSL 513  
 Db 481 QMOKLTNIITTEDIVVTWTVNVDPPPKESSL 513

RESULT 7  
 QJ1317  
 activin receptor precursor - African clawed frog  
 C:Species: Xenopus laevis (African clawed frog)  
 Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 18-Jun-1999  
 Accession: J01317  
 R:Kondo, M.; Tashiro, K.; Fujii, G.; Asano, M.; Miyoshi, R.; Yamada, R.; Muramatsu, M.;  
 Biochem. Biophys. Res. Commun. 181, 684-690, 1991  
 A:Title: Activin receptor mRNA is expressed early in Xenopus embryogenesis and the level  
 A:Reference number: J01317; MUID:92095974; PMID:1661587

A:Accession: J01317  
 A:Molecule type: mRNA  
 A:Residues: 1-514 <KON>  
 A:Cross-references: GB:S70930; NID:g240781; PIDN:AAB20638.1; PID:g240782  
 C:Superfamily: activin receptor II; protein kinase homology  
 C:Keywords: ATP; glycoprotein; serine/threonine-specific protein kinase; transmembrane  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-514/Product: activin receptor #status predicted <ACT>  
 F:137-162/Domain: transmembrane #status predicted <TRA>  
 F:191-487/Domain: protein kinase homology <KIN>  
 F:46,67,88,214,334/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match 89.6%; Score 2482.5; DB 2; Length 514;  
 Best Local Similarity 87.7%; Pred. No. 1.8e-126;  
 Matches 451; Conservative 37; Mismatches 25; Indels 1; Gaps 1;

Qy 1 MGAARKLAFVFLISCSGAILGRSETQCLFFNANWEKDRNTQGTGVEPCYGDKRRHC 59  
 Db 1 MGAATLALAVFLISCSGAILGRSETQCIYYNANWEKDKTNSNGTEICYGNDKRRHC 60  
 Qy 60 CFATWKNISGSIEIVKQGWLDLDCYDRDTCVEKKDSPEYVFCCCGNMCNEKFSYFPE 119  
 Db 61 CFATWKNISGSIEIVKQGWLDLDCYDRDTCIEKKDSPEYVFCCCGNMCNEKFSYFPE 120  
 Qy 120 MEVTOPTSNVTPKPPYYNILLISLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDPGP 179  
 Db 121 MEVTOPTSNVTPKPPYYNILLISLVPLIMVAVIVLFSFWMYRHHKLAYPPVLPVPTQDPGP 180  
 Qy 180 PPPSPILGLPLQLLEVKARGFCGVKQAQLNEYVAVKIFPIQDKOSWQNEVEYISLPG 239  
 Db 181 PPPSPILGLPLQLLEVKARGFCGVKQAQLNEYVAVKIFPIQDKOSWQNEVEYISLPG 240  
 Qy 240 GMKHNILQFIAEGRGTSVDVLDLITAFHEKGSLSDFLKANYVSNQLCHIAETMARG 299  
 Db 241 GMKHNILQFIAEGRGTSVDVLDLITAFHEKGSLSDFLKANYVSNNELCHIAETMARG 300  
 Qy 300 LAYLHEDIPGLKDGHPKPAISHRDIKSNVLLKNNLTACIADFGALALFEAGKSAGDTHGO 359  
 Db 301 LSHLHEDIPGLKDGHPKPAISHRDIKSNVLLKNNLTACIADFGALALFEAGKSAGDTHGO 360  
 Qy 360 VGTTRYMAPEVLEGAINFORDAFLRDMYAMGLVWLASRCTAAGDPVDEYMLPFEEI 419  
 Db 361 VGTTRYMAPEVLEGAINFORDAFLRDMYAMGLVWLASRCTAAGDPVDEYMLPFEEV 420  
 Qy 420 QHPSLEDQEVVVHKKRPVLRDYQKQHAGMAMLCETIEECWDHDAEARLSAGCVGERI 479  
 Db 421 QHPSLEDQEVVVHKKRPVLRDYQKQHAGMAMLCETIEECWDHDAEARLSAGCVGERI 480  
 Qy 480 TMORLTNIITTEDIVVTWTVNVDPPPKESSL 513  
 Db 481 IQOKLTNIITTEDIVVTWTVNVDPPPKESSL 514

RESULT 8  
 S21171  
 activin receptor STK9 - African clawed frog  
 C:Species: Xenopus laevis (African clawed frog)  
 C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 28-Feb-1997  
 C:Accession: S21171  
 R:Nishimatsu, S.; Oda, S.; Murakami, K.; Ueno, N.  
 FEBS Lett. 303, 81-84, 1992  
 A:Title: Multiple genes for Xenopus activin receptor expressed during early embryogen  
 A:Reference number: S21171; MUID:92275088; PMID:1317302

A:Accession: S21171  
 A:Molecule type: mRNA  
 A:Residues: 1-512 <NIS>  
 C:Superfamily: activin receptor II; protein kinase homology  
 C:Keywords: ATP  
 F:189-485/Domain: protein kinase homology <KIN>

Query Match 89.3%; Score 2474.5; DB 2; Length 512;  
 Best Local Similarity 86.9%; Pred. No. 4.8e-126;  
 Matches 446; Conservative 37; Mismatches 29; Indels 1; Gaps 1;

Qy 1 MGAARKLAFVFLISCSGAILGRSETQCLFFNANWEKDRNTQGTGVEPCYGDKRRHC 60  
 Db 1 MGAATLALAVFLIFCSGAILGRLETKCIYYNANWEKDKTNSNGTEPCYGDNDKRRHC 60  
 Qy 61 FATWKNISGSIEIVKQGWLDLDCYDRDTCVEKKDSPEYVFCCCGNMCNEKFSYFPEM 120  
 Db 61 FATWKNISGSIEIVKQGWLDLDCYDRDTCIEKKDSPEYVFCCCGNMCNEKFSYFPEM 120  
 Qy 121 EVTQPTSNVTPKPPYYNILLISLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDPGP 180  
 Db 121 EVTQPTSNVTPKPPYYNILLISLVPLIMVAVIVLFSFWMYRHHKLGYPPVLPVPTQDPGP 179  
 Qy 181 PPPSPILGLPLQLLEVKARGFCGVKQAQLNEYVAVKIFPIQDKOSWQNEVEYISLPG 240  
 Db 180 PPPSPILGLPLQLLEVKARGFCGVKQAQLNETVAVKIFPIQDKLSWQNEVEYISLPG 239

|    |     |   |     |
|----|-----|---|-----|
| Qy | 121 | EVQPTNSPVTPPPYNNILSYLVPLMLITAGVIGAFVYVYRHHKMAYPVPLVPTQDGP     | 180 |
| Db | 121 | ETFDPKPQ---PSASVNLNIIYSLLPVGLGSMALILAFWMYRHRKPPYGHVEI-NEDPGL  | 176 |
| Qy | 181 | PPSPLLGLAPQLLEVKARGGCVYKAOILLNYYAVKIFPIQDKQSQWQNEVYVSLPG      | 240 |
| Db | 177 | PPSPVLGLAPQLLETKARGGCVYKARLLNYYAVKIFPVQDKSQWQCEKEIFTTG        | 236 |
| Qy | 241 | MKHENILQFIAGKRGTSVDVLDWLITAPFHEKGSLSDFLKANYVSNOLCHIAETMARG    | 300 |
| Db | 237 | MKHENLLEETAAEKGSNLEWELWITAPHDKGSLLDYLGKLVSNWELCHITETMARG      | 296 |
| Qy | 301 | AYLHEDIPGLK-DGHRPAISHRODKSNVLLKNNLITACTADFLGALKFPAGKSAGDTHQ   | 359 |
| Db | 297 | AYLHEDYPRCKGEGHKAIAHRDFKSNVLLRDLTALADFLAVRFFPGPPGSDTHQ        | 356 |
| Qy | 360 | VGTRYMAPEVLEGAINFQDALFRIDMYAMGLVLMELASRCTAAGDPVDEYMLPFEERI    | 419 |
| Db | 357 | VGTRYMAPEVLEGAINFQDRSFLRIDMYAMGLVLMELVSVRCTAAGDPVDEYLLPFEERI  | 416 |
| Qy | 420 | GQHPLESLEDQEVVYVHKKRPVLRYQWKHAGMAMLCETIEECWDHDAEARLSAGCVGERI  | 479 |
| Db | 417 | GQHPLESLEDQEVVYVHKKIRPVFKDHLKHPGLAQLCVTIEECWDHDAEARLSAGCVGERI | 476 |
| Qy | 480 | TQMORLNIITTEDIVTVVMTVNTVNDPPPKRESSL                           | 513 |
| Db | 477 | SQIRKSVNGTTSDCGLVSIVTSVNTVNDLPPPKRESSI                        | 510 |

RESULT 10

A56926

activin receptor II STK3 precursor - African clawed frog

N:Alternate names: activin receptor 1

N:Contents: protein kinase STK3 (EC 2.7.1.-)

C:Species: xenopus laevis (African clawed frog)

C:Date: 08-Sep-1995 #sequence\_revision 19-Oct-1995 #text\_change 11-Jun-1999

C:Accession: A56926; S21234

R:Hemmati-Brivanlou, A.; Wright, D.A.; Melton, D.A. Dev. Dyn. 194, 1-11, 1992

A:Title: Embryonic expression and functional analysis of a Xenopus activin A:Reference number: A56926; MUID:93043515; PMID:1384808

A:Accession: A56926

A:Molecule type: mRNA

A:Residues: 1-510 <HEM>

A:Cross-references: GB:S49438; NID:g260043; PIDN:AAB24192.1; PID:g260044

A:Experimental source: oocytes

A:Note: sequence extracted from NCBI backbone (NCBIN:118655, NCBIF:118656)

R:Nishimatsu, S.; Oda, S.; Murakami, K.; Ueno, N. FEBS Lett. 303, 81-84, 1992

A:Title: Multiple genes for Xenopus activin receptor expressed during early A:Reference number: S21171; MUID:92275088; PMID:1317302

A:Accession: S21234

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-216, 'F', 218-478, 'I', 480-510 <NIS>

A:Experimental source: stage 5-6 embryos

C:Function:

C:Description: receptor for activin, which induces mesoderm formation in embryos

C:Superfamily: activin receptor II; protein kinase homology

C:Keywords: ATP; glycoprotein; phosphotransferase; receptor; serine/threonine

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-510/Product: activin receptor II #status predicted <MAT>

F:20-135/Domain: extracellular #status predicted <EXT>

F:136-157/Domain: transmembrane #status predicted <TM>

F:158-510/Domain: intracellular #status predicted <INT>

F:186-483/Domain: protein kinase homology <KIN>

F:195-202/Region: protein kinase ATP-binding motif

F:43,66/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:215/Active site: Lys #status predicted

|                       |        |                    |        |                |
|-----------------------|--------|--------------------|--------|----------------|
| Query Match           | 71.0%  | Score 1965.5;      | DB 1;  | Length 510;    |
| Best Local Similarity | 67.3%; | Pred. No. 1.1e-98; |        |                |
| Matches               | 346;   | Conservative       | 88;    | Mismatches 75; |
|                       |        |                    | Indels | 5;             |
|                       |        |                    | Gaps   |                |





QY 367 APEVLEGAINFQDAFLRIDMYAMGLVWELASRCTAADGPVDEYMLPFEETIGQHPSL 426  
Db 366 APEVLEGAINFQDAFLRIDMYAMGLVWELASRCTAADGPVDEYMLPFEETIGQHPSL 425  
QY 427 DMQEVVYVHKRPVLRDYWKHAGMAMLCETIECDWHDARLSAGCVGERITQMORLT 486  
Db 426 ELQEVVYVHKRPVLRDYWKHAGMAMLCETIECDWHDARLSAGCVGERITQMORLT 485  
QY 487 NIITTEDIVVTVMVTVNVDPPPKESSL 513  
Db 486 NGTSDCLVSLVTSVTVNVDLLPKESSI 512

RESULT 13  
A:0829  
activin receptor isoform IIB1 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 18-Jun-1999  
C:Accession: A40829  
R:Attisano, L.; Wrana, J.L.; Cheifetz, S.; Massague, J.  
Cell 68, 97-108, 1992  
A:Title: Novel activin receptors: distinct genes and alternative mRNA splicing generate  
A:Reference number: A40829; MUID:92119722; PMID:1310075  
A:Accession: A40829  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-536 <ATT>  
A:Experimental source: Balb/c 3T3  
A:Note: sequence inconsistent with the nucleotide translation  
C:Superfamily: activin receptor II; protein kinase homology  
C:Keywords: ATP; receptor; serine/threonine-specific protein kinase; transmembrane protein  
F:212-509/Domain: protein kinase homology <KIN>

Query Match 69.8%; Score 1934; DB 2; Length 536;  
Best Local Similarity 64.7%; Pred. No. 5.4e-97;  
Matches 343; Conservative 87; Mismatches 76; Indels 24; Gaps 2;

QY 8 AFVFLISCSGAILGRSETQECLEFFNANWEKDRNTQGVPECYGDKRHRHCFATWNI 67  
Db 7 ALALLWGSICAGSGRGAETRECIYNNANWELETRTQSGLERCEGQDKRLHCVASWRNS 66  
QY 68 SGSEIYVQGCWLDINCVDYDCEKDSPEVYFCCCEGNCMEKSFYFPEMEVTOPTS 127  
b 67 SGTIELVKKGCWLDNFCYDQECVATEENPQVYFCCCEGNCNERFTHLPFGPGPEVY 126  
QY 128 NPVTPEPPYNNILYSLVPLMIAIVICAFWYRHHKMAYPVVLV----- 173  
Db 127 EPPPTAPTLLTVLAYSLLPIGGSLIVLLAFWYRHKPPYGHVDIHEVRQCORWAGRRD 186  
QY 174 -----PTQDPGPPPPPLGLKPLQLEVKARGFCGVKWAQLLNEYVAVKIFPIQ 224  
Db 187 GCADSFPLFPDQPPPPPLVGLKPLQLEIKARGFCGVKWAQLLMDFVAVKIFPIQ 246  
QY 225 DKQSWQNEYVYSLPGMKHNIQLQFIAEKRGTSDVDLWLTAFHEKGSLSDFLKANYV 284  
Db 247 DKQSWQSERIEFTSPGKMHENLQFIAEKRGSNLEVLWLTAFHDKGSLTDYLGKNI 306  
QY 285 SWNOLCHIAETMARGLAYLHEDIPGLK-DGHPKPAISHRDIKSNVLLKNLTACIADFG 343  
Db 307 TWNELCHVAETMARGSLYHEDVPWCRGEGHKPSIAHRDFKSNVLLKSDLTAVLADFG 366  
QY 344 ALKFEAGKSADTHGVGTGRYNAPEVLEGAINFQDAFLRIDMYAMGLVWELASRCTA 403  
Db 367 AVFPEPKPGDTHGVGTGRYNAPEVLEGAINFQDAFLRIDMYAMGLVWELASRCTA 426  
QY 404 ADGPVDEYMLPFEETIGQHPSLDMQEVVYVHKRPVLRDYWKHAGMAMLCETIECDW 463  
Db 427 ADGPVDEYMLPFEETIGQHPSLDMQEVVYVHKRPVLRDYWKHAGMAMLCETIECDW 486  
QY 464 HDARLSAGCVGERITQMORLNIITTEDIVVTVMVTVNVDPPPKESSL 513  
Db 486 NGTSDCLVSLVTSVTVNVDLLPKESSI 512

Db 487 HDARLSAGCVGERVSLIRSVNGTSDCLVSLVTSVTVNVDLLPKESSI 536

RESULT 14  
A:0829  
activin receptor isoform IIB4 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-May-1997  
C:Accession: B40829  
R:Attisano, L.; Wrana, J.L.; Cheifetz, S.; Massague, J.  
Cell 68, 97-108, 1992  
A:Title: Novel activin receptors: distinct genes and alternative mRNA splicing genera  
A:Reference number: A40829; MUID:92119722; PMID:1310075  
A:Accession: B40829  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-504 <ATT>  
A:Experimental source: Balb/c 3T3  
A:Note: sequence inconsistent with the nucleotide translation  
C:Superfamily: activin receptor II; protein kinase homology  
C:Keywords: ATP; receptor  
F:180-477/Domain: protein kinase homology <KIN>

Query Match 69.4%; Score 1923; DB 2; Length 504;  
Best Local Similarity 67.1%; Pred. No. 2e-96;  
Matches 341; Conservative 88; Mismatches 67; Indels 12; Gaps 4;

QY 8 AFVFLISCSGAILGRSETQECLEFFNANWEKDRNTQGVPECYGDKRHRHCFATWNI 67  
Db 7 ALALLWGSICAGSGRGAETRECIYNNANWELETRTQSGLERCEGQDKRLHCVASWRNS 66  
QY 68 SGSEIYVQGCWLDINCVDYDCEKDSPEVYFCCCEGNCMEKSFYFPEMEVTOPTS 127  
Db 67 SGTIELVKKGCWLDNFCYDQECVATEENPQVYFCCCEGNCNERFTHLP----- 118  
QY 128 NPVTPEPPYNNILYSLVPLMIAIVICAFWYRHHKMAYPVVLVTPQDPGPPPPSPL 186  
Db 119 -PGPEAPTLLTVLAYSLLPIGGSLIVLLAFWYRHKPPYGHVDI-HEDEGPPPPSPL 176  
QY 187 LGLKPLQLEVKARGFCGVKWAQLLNEYVAVKIFPIQDKQSWQNEYVYSLPGMKHNI 246  
Db 177 VGLKPLQLEIKARGFCGVKWAQLLMDFVAVKIFPIQDKQSWQSERIEFTSPGKMHENL 236  
QY 247 LQFICAEKGTSDVDLWLTAFHEKGSLSDFLKANYVSNOLCHIAETMARGLAYLHED 306  
Db 237 LQFIAEKRGSNLEVLWLTAFHDKGSLTDYLGKNIITWNELCHVAETMARGSLYHED 296  
QY 307 IPGLK-DGHPKPAISHRDIKSNVLLKNLTACIADFGALALFEAGKSADTHGVGTGRY 365  
Db 297 VPCWCRGEGHKPSIAHRDFKSNVLLKSDLTAVLADFGLAVERFPGKPGDTHGVGTGRY 356  
QY 366 MAPEVLEGAINFQDAFLRIDMYAMGLVWELASRCTAADGPVDEYMLPFEETIGQHPSL 425  
Db 357 MAPEVLEGAINFQDAFLRIDMYAMGLVWELASRCTAADGPVDEYMLPFEETIGQHPSL 416  
QY 426 EDMQEVVYVHKRPVLRDYWKHAGMAMLCETIECDWHDARLSAGCVGERITQMORL 485  
Db 417 EELQEVVYVHKRPVLRDYWKHAGMAMLCETIECDWHDARLSAGCVGERVSLIRRS 476  
QY 486 TNIITTEDIVVTVMVTVNVDPPPKESSL 513  
Db 477 VNGTSDCLVSLVTSVTVNVDLLPKESSI 504

RESULT 15  
C:0829  
activin receptor isoform IIB3 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-May-1997  
C:Accession: C40829  
R:Attisano, L.; Wrana, J.L.; Cheifetz, S.; Massague, J.  
Cell 68, 97-108, 1992

A:Title: Novel activin receptors: distinct genes and alternative mRNA splicing generate

A:Reference number: A40829; MUID:92119722; PMID:1310075

A:Accession: C40829

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-528 <ATT>

A:Experimental source: Balb/c 3T3

A:Note: sequence inconsistent with the nucleotide translation

A:Note: sequence extracted from NCBI backbone (NCBIN:88362, NCBIIP:88363)

C:Superfamily: activin receptor II; protein kinase homology

C:Keywords: Atp; receptor

F:204-501/Domain: protein kinase homology <KIN>

Query Match 69.4%; Score 1922; DB 2; Length 528;

Best Local Similarity 64.6%; Pred. No. 2.4e-96;

Matches 343; Conservative 87; Mismatches 67; Indels 34; Gaps 4;

Qy 8 AFAYFLISCSGAILGRSETOECLEFFNANWEKDRNTQNGVEPCYGDKDKRRHCFATWKN I 67

Db 7 ALALLWSGLCAGSGEAEETRECIYYNANWELERTNOSGLERCEGEQDKRLHCYASWRNS 66

Qy 68 SGSEIVKQGCWLDDINCYDRTDCVEKKDSPEVYFCCEGNCMEKFSYPPEMEVTQPTS 127

Db 67 SGTIELVKKGCWLDDINCYDRTDCVEKKDSPEVYFCCEGNCMEKFSYPPEMEVTQPTS 118

Qy 128 NPVTPK-PPYNYNILLSVPLMLIAGIVICAFWYVYRHKKMAYPPVLV----- 173

Db 119 -PGGPEAPTLTLVLAYSLLPIGGLSLVLLAFWMYRHRKPPYGHVDIHEVRQCORWAGRR 177

Qy 174 -----PTQDPGPPPPSPILGLKPLQLLEVKARGFCGVWKAQLLNEYVAVKIFPI 223

Db 178 DGCADSFKPLPFQDPGPPSPILGLKPLQLLEIKARGFCGVWKAQLMNDFAVKIFPL 237

Qy 224 QDKQSWQNEYEVYSLPGMKHENILQFCAEKRGTSVDVLDLITAFHEKGSLSDFLKANV 283

Db 238 QDKQSWQSEREIFSTPGMKHENILQFCAEKRGTSVDVLDLITAFHEKGSLSDFLKANV 297

Qy 284 VSNOLCHIAETMARGLAYLHEDIPGLK-DGHKPAISHRDIKSKNVLKNNLTACIADFG 342

Db 298 ITWNELCVHAETMSRGLSYLHEDVPWCRGEGKPSIAHROFCKSNVLLKSDLTAVLADFG 357

Qy 343 LALKEACKSAGDTHGOVGTTRYWAPVLEGAINFORDAFLRIDMYAMGLVWELASRCT 402

Db 358 LAVRPECPKPGDTHGOVGTTRYWAPVLEGAINFORDAFLRIDMYAMGLVWELASRCT 417

Qy 403 AADGPVDEYMLPFEEIEGHPFLEDMQEVVYVKKRPVLRDYQKHAGMAMLCETIEECW 462

Db 418 AADGPVDEYMLPFEEIEGHPFLEDMQEVVYVKKRPVLRDYQKHAGMAMLCETIEECW 477

Qy 463 DHDAEARLSAGCVGRITQMORLTNITTEDIVTWVMTNVPFPPKESL 513

Db 478 DHDAEARLSAGCVGRITQMORLTNITTEDIVTWVMTNVPFPPKESL 528

Search completed: May 10, 2003, 18:00:11  
Job time : 23 secs

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: May 10, 2003, 18:00:15 ; Search time 91 Seconds  
(without alignments)  
1161.562 Million cell updates/sec

Title: US-09-742-684A-16  
Perfect score: 2770  
Sequence: 1 MGAARKLAFVFLISCSGA.....IVTVMTVNVDFPKESL 513

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPREMBL\_21.\*
- 2: sp\_archaea.\*
- 3: sp\_bacteria.\*
- 4: sp\_fungi.\*
- 5: sp\_human.\*
- 6: sp\_invertebrate.\*
- 7: sp\_mammal.\*
- 8: sp\_mhc.\*
- 9: sp\_organelle.\*
- 10: sp\_phage.\*
- 11: sp\_plant.\*
- 12: sp\_rodent.\*
- 13: sp\_virus.\*
- 14: sp\_vertebrate.\*
- 15: sp\_unclassified.\*
- 16: sp\_rvivirus.\*
- 17: sp\_bacteriap.\*
- 17: sp\_archaea.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result NO. | Score  | Query Match | Length | ID        | Description        |
|------------|--------|-------------|--------|-----------|--------------------|
| 1          | 2616   | 94.4        | 513    | 13 Q90669 | Q90669 gallus gall |
| 2          | 2604   | 94.0        | 513    | 13 Q90745 | Q90745 gallus gall |
| 3          | 2474.5 | 89.3        | 512    | 13 Q9PSM0 | Q9PSM0 xenopus lae |
| 4          | 2001   | 72.2        | 512    | 13 Q90670 | Q90670 gallus gall |
| 5          | 1975.5 | 71.3        | 510    | 13 Q9PSL8 | Q9PSL8 xenopus lae |
| 6          | 1971.5 | 71.2        | 510    | 13 Q9PSL9 | Q9PSL9 xenopus lae |
| 7          | 1965.5 | 71.0        | 510    | 13 Q91962 | Q91962 xenopus lae |
| 8          | 1872.5 | 67.6        | 509    | 13 Q9YGU4 | Q9YGU4 brachydanio |
| 9          | 1824   | 65.8        | 504    | 13 Q13102 | Q13102 carassius a |
| 10         | 1500   | 54.2        | 292    | 13 Q9PSG1 | Q9PSG1 gallus gall |
| 11         | 1312.5 | 47.4        | 365    | 13 Q91347 | Q91347 xenopus lae |
| 12         | 1312.5 | 47.4        | 386    | 13 Q9PSL7 | Q9PSL7 xenopus lae |
| 13         | 1150.5 | 41.5        | 516    | 5 Q24468  | Q24468 drosophila  |
| 14         | 1147.5 | 41.4        | 516    | 5 Q24229  | Q24229 drosophila  |
| 15         | 1071   | 38.7        | 254    | 6 P79233  | P79233 papio hamad |
| 16         | 1034.5 | 37.3        | 233    | 13 Q9PSG2 | Q9PSG2 gallus gall |

|    |       |      |      |           |                     |
|----|-------|------|------|-----------|---------------------|
| 17 | 996   | 36.0 | 262  | 6 Q95L45  | Q95L45 ovis aries   |
| 18 | 975   | 35.2 | 175  | 11 Q64209 | Q64209 rattus sp.   |
| 19 | 913   | 33.0 | 175  | 6 Q9GLC1  | Q9GLC1 sus scrofa   |
| 20 | 886   | 32.0 | 159  | 6 Q95JA7  | Q95JA7 oryctolagus  |
| 21 | 882.5 | 31.9 | 284  | 5 Q95T01  | Q95T01 drosophila   |
| 22 | 789.5 | 28.5 | 557  | 13 Q90999 | Q90999 gallus gall  |
| 23 | 779   | 28.1 | 567  | 11 Q91288 | Q91288 mus musculus |
| 24 | 775.5 | 28.0 | 530  | 4 Q13161  | Q13161 homo sapien  |
| 25 | 774.5 | 28.0 | 567  | 6 Q9TS29  | Q9TS29 mustela sp.  |
| 26 | 749.5 | 27.1 | 1048 | 13 P79954 | P79954 xenopus lae  |
| 27 | 748   | 27.0 | 1031 | 13 Q42124 | Q42124 gallus gall  |
| 28 | 733   | 26.5 | 534  | 13 Q9DE31 | Q9DE31 xenopus lae  |
| 29 | 706.5 | 25.5 | 903  | 5 Q9NGX8  | Q9NGX8 drosophila   |
| 30 | 703.5 | 25.4 | 903  | 5 Q95V83  | Q95V83 drosophila   |
| 31 | 703.5 | 25.4 | 903  | 5 Q9VZ19  | Q9VZ19 drosophila   |
| 32 | 664   | 24.0 | 532  | 11 Q64308 | Q64308 rattus norv  |
| 33 | 662.5 | 23.9 | 527  | 13 Q42338 | Q42338 xenopus lae  |
| 34 | 662.5 | 23.9 | 527  | 13 Q91578 | Q91578 xenopus lae  |
| 35 | 656.5 | 23.7 | 533  | 13 Q9PUF5 | Q9PUF5 coturnix co  |
| 36 | 656.5 | 23.7 | 533  | 13 Q90754 | Q90754 gallus gall  |
| 37 | 655.5 | 23.7 | 527  | 13 Q42339 | Q42339 xenopus lae  |
| 38 | 653.5 | 23.6 | 502  | 6 Q9BD14  | Q9BD14 ovis aries   |
| 39 | 653.5 | 23.6 | 502  | 11 Q9QVT7 | Q9QVT7 rattus sp.   |
| 40 | 651.5 | 23.5 | 502  | 6 Q95L23  | Q95L23 sus scrofa   |
| 41 | 650   | 23.5 | 974  | 5 Q9UAG0  | Q9UAG0 ephydratia f |
| 42 | 640   | 23.1 | 530  | 13 Q9W629 | Q9W629 brachydanio  |
| 43 | 639.5 | 23.1 | 493  | 4 Q8TBG2  | Q8TBG2 homo sapien  |
| 44 | 638   | 23.0 | 500  | 13 Q91595 | Q91595 xenopus lae  |
| 45 | 637.5 | 23.0 | 493  | 11 P70539 | P70539 rattus norv  |

## ALIGNMENTS

## RESULT 1

Q90669 ID Q90669 PRELIMINARY; PRT; 513 AA.  
 AC Q90669;  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
 DE 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
 DE Activin receptor IIA.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96069914; PubMed=7589799;  
 RA Stern C.D., Yu R.T., Kakizuka A., Kintner C.R., Mathews L.S.,  
 RA Vale W.W., Evans R.M., Umesono K.;  
 RT "Activin and its receptors during gastrulation and the later phases of  
 RT mesoderm development in the chick embryo.";  
 RL Dev. Biol. 172:192-205(1995).  
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; U31222; AAA87841.1;  
 DR HSSP; P27038; IRTS.  
 DR InterPro; IPR000472; Activin\_rec.  
 DR InterPro; IPR000333; Actn\_receptorII.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF01064; Activin\_rec; 1.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00653; ACTIVIN2R.  
 DR ProDom; PD000001; Euk\_pkinase; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_SF; 1.  
 KW ATP-binding; Receptor; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 513 AA; 58092 MW; 03128AB7FF732552 CRC64;

Query Match 94.4%; Score 2616; DB 13; Length 513;  
 Best Local Similarity 92.4%; Pred. No. 7.1e-236;

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Matches 474; Conservative 28; Mismatches 11; Indels 0; Gaps 0;
Qy 1 MGAATKALFAVELISCSSGAILGRSETQECLEFFNANWEKDRNTQGTGPEYCGDKRRHC 60
Db 1 MGAATKALFAVELISCSSGAILGRSETQECLEFFNANWEKDRNTQGTGPEYCGDKRRHC 60
Qy 61 FATWKNISGSIIEVKQGCWLLDDINCYDRDTCVCKKSDPEVYFCCCEGNMCKNEKFSYFPEM 120
Db 61 FATWKNISGSIIEVKQGCWLLDDINCYDRDTCVCKKSDPEVYFCCCEGNMCKNEKFSYFPEM 120
Qy 121 EVTQPTSNPVTPKPPYNYLLISLVPLMLTAGIVICAFWYRHHKMAYPVLPVPTQDPGP 180
Db 121 EVTQPTSNPVTPKPPYNYLLISLVPLMLTAGIVICAFWYRHHKMAYPVLPVPTQDPGP 180
Qy 181 PPPPLGLKPLQLLEVKARGFCVWKAQLNEYVAVKIFPIQDKQSWONEVEYISLPG 240
Db 181 PPPPLGLKPLQLLEVKARGFCVWKAQLNEYVAVKIFPIQDKQSWONEVEYISLPG 240
Qy 241 MKHENILQFIAEGRKTSIDVDLMLITAFHEKGSLSDFLKNVYVSNWOLCHIAETMARGL 300
Db 241 MKHDNILQFIAEGRKTSIDVDLMLITAFHEKGSLSDFLKNVYVSNWELCHIAQTMRGL 300
Qy 301 AYLEDIPGLKDGHPAISHRDIKSNVLLKNNLTACIADFGALKEAGKSAGDTHGOV 360
Db 301 AYLEDIPGLKDGHPAISHRDIKSNVLLKNNLTACIADFGALKEAGKSAGDTHGOV 360
Qy 361 GTRRYMAPEVLEGAINFORDAFLRIDMYAGLVWELASRCTAADGPVDEYMLPFEEIG 420
Db 361 GTRRYMAPEVLEGAINFORDAFLRIDMYAGLVWELASRCTASDGPVDEYMLPFEEIG 420
Qy 421 QHPSEDMQEVVYVHKRPVLRDYQWKHAGMAMLCETIEECWDHDAEARSAGCVGERIT 480
Db 421 QHPSEDMQEVVYVHKRPVLRDYQWKHAGMAMLCETIEECWDHDAEARSAGCVGERII 480
Qy 481 QMOKLTNIITTEDIVTVVMTNVDPPKESL 513
Db 481 QMOKLTNIITTEDIVTVVMTNVDPPKESL 513
RESULT 2
Q90745 PRELIMINARY; PRT; 513 AA.
AC Q90745;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Activin receptor, type IIA.
GN ACTIVIN RECEPTOR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
[1]
SEQUENCE FROM N.A.
MEDLINE=92299088; PubMed=1318847;
Chuchi H., Noji S., Koyama E., Miyokai F., Nishikawa K., Nohno T.,
Tashiro K., Shikawa K., Matsuo N., Taniguchi S.;
"Expression pattern of the activin receptor type IIA gene during
differentiation of chick neural tissues, muscle and skin.";
FEBS Lett. 303:185-189(1992).
[2]
SEQUENCE FROM N.A.
Nohno T.;
"None.";
Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: D31899; BAA06697.1; -.
DR HSSP: P27038; 1BTE.
DR InterPro: IPR000472; Activin_rec.
DR InterPro: IPR000333; Actn_receptorII.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_kinase.
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DR Pfam: PF01064; Activin_rec; 1.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00653; Activin2R.
DR ProDom: PD00001; Euk_pkinase; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Receptor; Serine/threonine-protein kinase; Transferase.
KW SEQUENCE 513 AA; 57923 MW; EIB4B8A076C41B80 CRC64;
Query Match 94.0%; Score 2604; DB 13; Length 513;
Best Local Similarity 92.2%; Pred. NO. 9.4e-235;
Matches 473; Conservative 26; Mismatches 14; Indels 0; Gaps 0;
Qy 1 MGAATKALFAVELISCSSGAILGRSETQECLEFFNANWEKDRNTQGTGPEYCGDKRRHC 60
Db 1 MGAATKALFAVELISCSSGAILGRSETQECLEFFNANWEKDRNTQGTGPEYCGDKRRHC 60
Qy 61 FATWKNISGSIIEVKQGCWLLDDINCYDRDTCVCKKSDPEVYFCCCEGNMCKNEKFSYFPEM 120
Db 61 FATWKNISGSIIEVKQGCWLLDDINCYDRDTCVCKKSDPEVYFCCCEGNMCKNEKFSYFPEM 120
Qy 121 EVTQPTSNPVTPKPPYNYLLISLVPLMLTAGIVICAFWYRHHKMAYPVLPVPTQDPGP 180
Db 121 EVTQPTSNPVTPKPPYNYLLISLVPLMLTAGIVICAFWYRHHKMAYPVLPVPTQDPGP 180
Qy 181 PPPPLGLKPLQLLEVKARGFCVWKAQLNEYVAVKIFPIQDKQSWONEVEYISLPG 240
Db 181 PPPPLGLKPLQLLEVKARGFCVWKAQLNEYVAVKIFPIQDKQSWONEVEYISLPG 240
Qy 241 MKHENILQFIAEGRKTSIDVDLMLITAFHEKGSLSDFLKNVYVSNWOLCHIAETMARGL 300
Db 241 MKHDNILQFIAEGRKTSIDVDLMLITAFHEKGSLSDFLKNVYVSNWELCHIAQTMRGL 300
Qy 301 AYLEDIPGLKDGHPAISHRDIKSNVLLKNNLTACIADFGALKEAGKSAGDTHGOV 360
Db 301 AYLEDIPGLKDGHPAISHRDIKSNVLLKNNLTACIADFGALKEAGKSAGDTHGOV 360
Qy 361 GTRRYMAPEVLEGAINFORDAFLRIDMYAGLVWELASRCTAADGPVDEYMLPFEEIG 420
Db 361 GTRRYMAPEVLEGAINFORDAFLRIDMYAGLVWELASRCTASDGPVDEYMLPFEEIG 420
Qy 421 QHPSEDMQEVVYVHKRPVLRDYQWKHAGMAMLCETIEECWDHDAEARSAGCVGERIT 480
Db 421 QHPSEDMQEVVYVHKRPVLRDYQWKHAGMAMLCETIEECWDHDAEARSAGCVGERII 480
Qy 481 QMOKLTNIITTEDIVTVVMTNVDPPKESL 513
Db 481 QMOKLTNIITTEDIVTVVMTNVDPPKESL 513
RESULT 3
Q9PSM0 PRELIMINARY; PRT; 512 AA.
AC Q9PSM0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Activin RECEPTOR-CLONE XSf9.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=6355;
[1]
SEQUENCE FROM N.A.
MEDLINE=92275088; PubMed=1317302;
Nishimatsu S., Oda S., Murakami K., Ueno N.;
"Multiple genes for Xenopus activin receptor expressed during early
embryogenesis.";
FEBS Lett. 303:81-84(1992).
CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR HSSP: P27038; 1BTE.
DR InterPro: IPR000472; Activin_rec.
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DR InterPro; IPR000333; Actn_receptorII.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF01064; Actiniv_rec; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00653; ACTININ2R.
DR PRINTS; PR00653; ACTININ2R.
DR PRODOM; PD000001; Euk_pkinase; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Serine/threonine-protein kinase; Transferase.
KW SEQUENCE 512 AA; 57819 MW; B784BD1B52D506F3 CRC64;

Query Match      89.3%; Score 2474.5; DB 13; Length 512;
Best Local Similarity 86.9%; Pred. No. 1.2e-222;
Matches 446; Conservative 37; Mismatches 29; Indels 1; Gaps 1;

QY 1 MGAATKLAFAVFLISCSGAILGRSETQECLEFFNANWEKDRNTQTVGPCYGDKRRHCF 60
DB 1 MGAATKLAFAVFLISCSGAILGRSETQECLEFFNANWEKDRNTQTVGPCYGDKRRHCF 60
QY 61 FATWKNISGSTEIVKQCGWLDLDCYDRTDCVEKKDSPEYVFCCEGNCNEKFSYFPEM 120
DB 61 FATWKNISGSTEIVKQCGWLDLDCYDRTDCVEKKDSPEYVFCCEGNCNEKFSYFPEM 120
QY 121 EVTQPTNSPVTPKPPYNYLLISLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDGP 180
DB 121 EVTQPTNSPVTPKPPYNYLLISLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDGP 180
QY 181 PPSPLGLPLQLLEVKARGFCGVWKAQLNEYVAVKIFPIQDKOSQWNEYEVYSLFG 240
DB 181 PPSPLGLPLQLLEVKARGFCGVWKAQLNEYVAVKIFPIQDKOSQWNEYEVYSLFG 240
QY 241 MKHENILQFCAEKGRTSVDDVLDLITAFHEKGSLSDFLKANVVSNNQLCHTAETMARG 300
DB 241 MKHENILQFCAEKGRTSVDDVLDLITAFHEKGSLSDFLKANVVSNNQLCHTAETMARG 300
QY 301 AYLEDIPGLKGDGHPAISHRDIKSNVLLKNNLTACIADFGALKEAGKSAGDTHGV 360
DB 301 AYLEDIPGLKGDGHPAISHRDIKSNVLLKNNLTACIADFGALKEAGKSAGDTHGV 360
QY 361 GTRYMAPEVLEGAINFOADFLRIDMYAGLVWLWELASRCTAADGPVDEYMLPFEETG 420
DB 361 GTRYMAPEVLEGAINFOADFLRIDMYAGLVWLWELASRCTAADGPVDEYMLPFEETG 420
QY 421 QHPSLEDQEVVYVHKRPRVLDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480
DB 421 QHPSLEDQEVVYVHKRPRVLDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480
QY 481 QMORLNIITTEDIVTVVTMTNVDPPPKESSL 513
DB 481 QMORLNIITTEDIVTVVTMTNVDPPPKESSL 513

RESULT 4
Q90670 ID Q90670 PRELIMINARY; PRT; 512 AA.
AC Q90670;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Activin receptor IIB.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96069914; PubMed=7589799;
RA Stern C.D., Yu R.T., Kakizuka A., Kintner C.R., Mathews L.S.,
Vale W.W., Evans R.M., Umesono K.;

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RT "Activin and its receptors during gastrulation and the later phases of
RT mesoderm development in the chick embryo.";
RL Dev. Biol. 172:192-205(1995).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; U31223; AAA87842.1; -.
DR HSP; P27038; 1BTE.
DR InterPro; IPR000472; Actiniv_rec.
DR InterPro; IPR000333; Actn_receptorII.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF01064; Actiniv_rec; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00653; ACTININ2R.
DR PRODOM; PD000001; Euk_pkinase; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Receptor; Serine/threonine-protein kinase; Transferase.
KW SEQUENCE 512 AA; 57776 MW; 6051FOCB9E4AE060 CRC64;

Query Match      72.2%; Score 2001; DB 13; Length 512;
Best Local Similarity 68.9%; Pred. No. 2.4e-178;
Matches 353; Conservative 80; Mismatches 77; Indels 2; Gaps 2;

QY 3 AAATKLAFAVFLISCSGAILGRSETQECLEFFNANWEKDRNTQTVGPCYGDKRRHCF 62
DB 3 AAATKLAFAVFLISCSGAILGRSETQECLEFFNANWEKDRNTQTVGPCYGDKRRHCF 62
QY 63 TWKNISGSTEIVKQCGWLDLDCYDRTDCVEKKDSPEYVFCCEGNCNEKFSYFPEM 122
DB 63 TWKNISGSTEIVKQCGWLDLDCYDRTDCVEKKDSPEYVFCCEGNCNEKFSYFPEM 122
QY 123 TQPTNSPVTPKPPYNYLLISLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDGP 182
DB 123 TQPTNSPVTPKPPYNYLLISLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDGP 182
QY 183 PPSPLGLPLQLLEVKARGFCGVWKAQLNEYVAVKIFPIQDKOSQWNEYEVYSLFG 242
DB 183 PPSPLGLPLQLLEVKARGFCGVWKAQLNEYVAVKIFPIQDKOSQWNEYEVYSLFG 242
QY 243 HENILQFCAEKGRTSVDDVLDLITAFHEKGSLSDFLKANVVSNNQLCHTAETMARG 302
DB 243 HENILQFCAEKGRTSVDDVLDLITAFHEKGSLSDFLKANVVSNNQLCHTAETMARG 302
QY 303 LHEDIPGLKGDGHPAISHRDIKSNVLLKNNLTACIADFGALKEAGKSAGDTHGV 361
DB 303 LHEDIPGLKGDGHPAISHRDIKSNVLLKNNLTACIADFGALKEAGKSAGDTHGV 361
QY 361 GTRYMAPEVLEGAINFOADFLRIDMYAGLVWLWELASRCTAADGPVDEYMLPFEETG 421
DB 361 GTRYMAPEVLEGAINFOADFLRIDMYAGLVWLWELASRCTAADGPVDEYMLPFEETG 421
QY 422 QHPSLEDQEVVYVHKRPRVLDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 481
DB 422 QHPSLEDQEVVYVHKRPRVLDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 481
QY 481 QMORLNIITTEDIVTVVTMTNVDPPPKESSL 513
DB 481 QMORLNIITTEDIVTVVTMTNVDPPPKESSL 513

RESULT 5
Q9PSL8 ID Q9PSL8 PRELIMINARY; PRT; 510 AA.
AC Q9PSL8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Activin RECEPTOR-CLONE XSTK3.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;

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RN  SEQUENCE FROM N.A.
RX  MEDLINE=9275088; PubMed=1317302;
RA  Nishimatsu S., Oda S., Murakami K., Ueno N.;
RT  "Multiple genes for Xenopus activin receptor expressed during early
RT  embryogenesis.";
RL  FEBS Lett. 303:81-84(1992).
CC  -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR  HSSP; P27038; 18TE.
DR  InterPro; IPR000472; Actin_rec.
DR  InterPro; IPR000333; Actn_receptorII.
DR  InterPro; IPR000719; Euk_pkinase.
DR  InterPro; IPR002290; Ser_thr_pkinase.
DR  InterPro; IPR001245; Tyr_pkinase.
DR  Pfam; PF01064; Activin_rec; 1.
DR  Pfam; PF00069; pkinase; 1.
DR  PRINTS; PR00653; ACTIVIN2R.
DR  PRINTS; PR00109; TYRKINASE.
DR  ProDom; PD000001; Euk_pkinase; 1.
DR  ProSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR  ProSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW  ATP-binding; Serine/threonine-protein kinase; Transferase.
SQ  SEQUENCE 510 AA; 57852 MW; 3CD03B6A48953067 CRC64;

Query Match 71.3%; Score 1975.5; DB 13; Length 510;
Best Local Similarity 67.5%; Pred. No. 5.8e-176;
Matches 347; Conservative 89; Mismatches 73; Indels 5; Gaps 3;

QY  1 MGAATAAFVAVFLVSSCGAILGRSETQCLFFNANWEKDRDTNQTGVEPCYGDKKRRHC 60
DB  1 MGAAYPLTLALLATFRAGSGHDEVEETRECIYNNANWELEKTNQSGVCEGDKRLHC 60
QY  61 FATKNISGSIEIVKQGCWLDINCYDRTDCVEKKDPSVEYFCCCEGNCNKEKSFYFPEM 120
DB  61 YASWRNNSGFIELVKGCWLDNFCYDQECIAKEENPQVFCCCEGNCNKKFTHLPEV 120
QY  121 EYVQTSNPVTPKPPYNYLLISLVPLMLIAGIVICAFWYRHHKMAPVPLVPTQDGP 180
DB  121 EYFDPKPPM---PSVLNLIYSLPIAGLSNVLIAFWYRHHKPPYGHVDL-NEDPGP 176
QY  181 PPSPLGLKPLQLLEVKARGGCVKQALLNEVAVKIFPIODKQSWONEYEYVSLPG 240
DB  177 TPSPWVGLKPLQLLEIKARGGCVKARLLNEVAVKIFPVQDKQSWOCEKEIFNTPG 236
QY  241 MKHENILOFAGKRGTSVDVLDLWITAFHEKGSLSDFLKANYVSWNOLCHIAETMARGL 300
DB  237 MKHENLEFIAEKRGSNLEMLWLITAFHDKGSLTDYLGKLVNWNELCHITETMARGL 296
QY  301 AYLEDIPGLK-DGHPAISHRDIKSNVLLKNNLTACIADFGALKFEAGKSAGDTHGQ 359
DB  297 SYLHEDVPRCKGEGHKAHRAHDFKSNVLRNDLTALADFGLAVERPEKPPGDTHGQ 356
QY  360 VGTTRYMAPEVLEGAINFORDAFLRDMYAGLVLMWELASRCTAADGPVDEYMLPFEEI 419
DB  357 VGTTRYMAPEVLEGAINFORDFLRDMYAGLVLMWELVSVSCTAADGPVDEYMLPFEEI 416
QY  420 GQHPLEDQEVVYVHKRPVLDYQKQKAGMAMLCETIEECWDHDAEARLSAGCVGERI 479
DB  417 GQHPLEDLQEVVYVHKRPVFKDHLKHPGLAQLCVITIEECWDHDAEARLSAGCVGERI 476
QY  480 TOMQRLTNITTEDIVTVVTVNVDPPKESL 513
DB  477 SQIRKSVNGTTSDCLSIVTSVTVNVDLPKESSI 510

RESULT 6
Q9PSL9 PRELIMINARY; PRT; 510 AA.
AC Q9PSL9;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAY-2002 (Tremblrel. 20, Last annotation update)
DE Activin RECEPTOR-CLONE xSTR8.

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OS  Xenopus laevis (African clawed frog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC  Xenopodinae; Xenopus.
OX  NCBI_TaxID=8355;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=9275088; PubMed=1317302;
RA  Nishimatsu S., Oda S., Murakami K., Ueno N.;
RT  "Multiple genes for Xenopus activin receptor expressed during early
RT  embryogenesis.";
RL  FEBS Lett. 303:81-84(1992).
CC  -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR  HSSP; P27038; 18TE.
DR  InterPro; IPR000472; Actin_rec.
DR  InterPro; IPR000333; Actn_receptorII.
DR  InterPro; IPR000719; Euk_pkinase.
DR  InterPro; IPR002290; Ser_thr_pkinase.
DR  Pfam; PF01064; Activin_rec; 1.
DR  Pfam; PF00069; pkinase; 1.
DR  PRINTS; PR00653; ACTIVIN2R.
DR  ProDom; PD000001; Euk_pkinase; 1.
DR  ProSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR  ProSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW  ATP-binding; Serine/threonine-protein kinase; Transferase.
SQ  SEQUENCE 510 AA; 57782 MW; 99C7567C19F29992 CRC64;

Query Match 71.2%; Score 1971.5; DB 13; Length 510;
Best Local Similarity 67.9%; Pred. No. 1.4e-175;
Matches 349; Conservative 85; Mismatches 75; Indels 5; Gaps 3;

QY  1 MGAATAAFVAVFLVSSCGAILGRSETQCLFFNANWEKDRDTNQTGVEPCYGDKKRRHC 60
DB  1 MGAVALTFLLLATFRAGSGHDEVEETRECIYNNANWELEKTNQSGVCEGDKRLHC 60
QY  61 FATKNISGSIEIVKQGCWLDINCYDRTDCVEKKDPSVEYFCCCEGNCNKEKSFYFPEM 120
DB  61 YASWRNNSGFIELVKGCWLDNFCYDQECIAKEENPQVFCCCEGNCNKKFTHLPEV 120
QY  121 EYVQTSNPVTPKPPYNYLLISLVPLMLIAGIVICAFWYRHHKMAPVPLVPTQDGP 180
DB  121 EYFDPKPPQ---PSASVLNLIYSLPIVGLSMAILAFWYRHHKPPYGHVEI-NEDPGL 176
QY  181 PPSPLGLKPLQLLEVKARGGCVKQALLNEVAVKIFPIODKQSWONEYEYVSLPG 240
DB  177 PPSPLVGLKPLQLLEIKARGGCVKARLLNEVAVKIFPVQDKQSWOCEKEIFNTPG 236
QY  241 MKHENILOFAGKRGTSVDVLDLWITAFHEKGSLSDFLKANYVSWNOLCHIAETMARGL 300
DB  237 MKHENLEFIAEKRGSNLEMLWLITAFHDKGSLTDYLGKLVNWNELCHITETMARGL 296
QY  301 AYLEDIPGLK-DGHPAISHRDIKSNVLLKNNLTACIADFGALKFEAGKSAGDTHGQ 359
DB  297 AYLEDVPRCKGEGHKAHRAHDFKSNVLRNDLTALADFGLAVERPEKPPGDTHGQ 356
QY  360 VGTTRYMAPEVLEGAINFORDAFLRDMYAGLVLMWELASRCTAADGPVDEYMLPFEEI 419
DB  357 VGTTRYMAPEVLEGAINFORDFLRDMYAGLVLMWELVSVSCTAADGPVDEYMLPFEEI 416
QY  420 GQHPLEDQEVVYVHKRPVLDYQKQKAGMAMLCETIEECWDHDAEARLSAGCVGERI 479
DB  417 GQHPLEDLQEVVYVHKRPVFKDHLKHPGLAQLCVITIEECWDHDAEARLSAGCVGERI 476
QY  480 TOMQRLTNITTEDIVTVVTVNVDPPKESL 513
DB  477 SQIRKSVNGTTSDCLSIVTSVTVNVDLPKESSI 510

RESULT 7
Q91962 PRELIMINARY; PRT; 510 AA.
ID Q91962
AC Q91962;
DT 01-NOV-1996 (Tremblrel. 01, Created)

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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Activin receptor.  
 OS Xenopus.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Eupidae;  
 OC Xenopodinae.  
 NCBI\_TaxID=8353;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93043515; PubMed=1384808;  
 RA Hemmati-Brivanlou A., Wright D.A., Melton D.A.;  
 RT "Embryonic expression and functional analysis of a xenopus activin  
 receptor.";  
 RL Dev. Dyn. 194:1-11(1992).  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; S49438; AAB24192.1; -;  
 DR HSP; P27038; ISTE.  
 DR InterPro; IPR000472; Activin\_rec.  
 DR InterPro; IPR000333; Actn\_receptorII.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF01064; Activin\_rec; 1.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00653; ACTIVIN2R.  
 DR ProDom; PD000001; Euk\_pkinase; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Receptor; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 510 AA; 57780 MW; C6C07B6A42236A0 CRC64;  
 Query Match 71.0%; Score 1965.5; DB 13; Length 510;  
 Best Local Similarity 67.3%; Pred. No. 5e-175;  
 Matches 346; Conservative 88; Mismatches 75; Indels 5; Gaps 3;  
 QY 1 MGAALAPAVFLISCGSAILGRSETOECLFFNANWEKDRNTQTVGPCYGDGKRRHC 60  
 Db 1 MGAAPVLTALLATFADPSHGEVETRECIYNNANWELEKTNQSGVECEGEKRLHC 60  
 QY 61 FATWKNISGIEVKGWGLDDINCYDRTDCVEKKDSPEVYFCCCGNMCNEKFSYFPEM 120  
 Db 61 YASWRNNSGFIELVKGWGLDDINCYDQECIAKENPQVFFCCCGNMCNEKFSYFPEM 120  
 QY 121 EVTQTSNPVTPKPPYNNILYSLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTDQGP 180  
 Db 121 ETDPKQPM--PSVLNIIYSLPLIAGLSWVILLAFWYRHHKPPYGHVDL-NEDPGP 176  
 QY 181 PPPSLGLKPLQLLEKARGGCVKQAQLNEYVAVKIFPIODKQSNQNEYEVYSLPG 240  
 Db 177 TFPSPWGLKPLQLLEKARGGCVKQAQLNEYVAVKIFPIODKQSNQNEYEVYSLPG 236  
 QY 241 MKHENILOFTGAERKGTSDVDLWLITAFHEKGSLSDFLKANVSWNOLCHIAETMARG 300  
 Db 237 MKHENILEFTAAEKGSNLEMLWLITAFHDKGSLTDYLGKLVNWNELCHITETMARG 296  
 QY 301 AYLEDIPGLK-DGHKPAISHRDKSKNVLKNNLTACTADFLGALKFAGKSAGDTHQ 359  
 Db 297 SYLHEDVPKCGKHGKPAIAHRDFKSKNVLIRNDLTAILADFLGALVRFPPGPDTHQ 356  
 QY 360 VGTFRYMAPVLEGAINFOADFLRDMYAMGLVWELASRCTAADGPVDEYMLPFEEI 419  
 Db 357 VGTFRYMAPVLEGAINFOADFLRDMYAMGLVWELASRCTAADGPVDEYMLPFEEI 416  
 QY 420 GQPSLEDQEVVYVHKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCVGERI 479  
 Db 417 GQPSLEDQEVVYVHKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCVGERI 476  
 QY 480 TQMRITNITTEDIVVTMTNVDPPKESL 513  
 Db 477 SQRKSVNGTSDCLSVISVTSNTVDLPKESI 510

RESULT 8

QYVGUA  
 ID Q9YGU4 PRELIMINARY; PRT; 509 AA.  
 AC Q9YGU4;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Activin receptor IIB.  
 GN ACVR2B OR ACTRIIB.  
 OS Brachydanio rerio (zebrafish) (Zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99387621; PubMed=10459865;  
 RA Garg R.R., Bally-Cuif L., Lee S.E., Gong Z., Ni X., Hew C.L., Peng C.;  
 RT "Cloning of zebrafish activin type IIB receptor (ActRIIB) cDNA and  
 mRNA expression of ActRIIB in embryos and adult tissues.";  
 RL Mol. Cell. Endocrinol. 153:169-181(1999).  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; AF069500; AAD19844.1; -;  
 DR HSP; P27038; ISTE.  
 DR ZFIN; ZDB-GENE-980526-549; acvr2b.  
 DR InterPro; IPR000472; Activin\_rec.  
 DR InterPro; IPR000333; Actn\_receptorII.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF01064; Activin\_rec; 1.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00653; ACTIVIN2R.  
 DR ProDom; PD000001; Euk\_pkinase; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Receptor; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 509 AA; 57478 MW; B07E30E076C9E373 CRC64;  
 Query Match 67.6%; Score 1872.5; DB 13; Length 509;  
 Best Local Similarity 65.6%; Pred. No. 2.5e-166;  
 Matches 335; Conservative 87; Mismatches 84; Indels 5; Gaps 4;  
 QY 4 AAKLAFVFLISCGSAILGRSETOECLFFNANWEKDRNTQTVGPCYGDGKRRHC 63  
 Db 3 ASLLTALLATFADPSHGEVETRECIYNNANWELEKTNQSGVECEGEKRRHC 62  
 QY 64 WKNISGSIETVKGWGLDDINCYDRTDCVEKKDSPEVYFCCCGNMCNEKFSYFPEM 123  
 Db 63 WRNNSGSIETVKGWGLDDINCYDQECIAKENPQVFFCCCGNMCNEKFSYFPEM 120  
 QY 124 OPTSNPTVPKPPYNNILYSLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTDQGP 183  
 Db 121 GPVTSPPVPSLNLVILVSLPLSLMFLAFWYRHHKPPYGHVDV-NEDPGP 179  
 QY 184 SPLGLKPLQLLEKARGGCVKQAQLNEYVAVKIFPIODKQSNQNEYEVYSLPGMKH 243  
 Db 180 SPLVGLKPLQLLEKARGGCVKQAQLNEYVAVKIFPIODKQSNQNEYEVYSLPGMKH 239  
 QY 244 ENILOFTGAERKGTSDVDLWLITAFHEKGSLSDFLKANVSWNOLCHIAETMARG 303  
 Db 240 DNLLRFIAAERKGSNLEMLWLITAFHDKGSLTDYLGKLVNWNELCHITETMARG 299  
 QY 304 HEDIPGLK-DGHKPAISHRDKSKNVLKNNLTACTADFLGALKFAGKSAGDTHQ 362  
 Db 300 HEDVPSRSGEGKPAIAHRDFKSKNVLMDLTAVIGDGLVAFEPKPGPDTHQ 359  
 QY 363 RRYMAPEVLEGAINFOADFLRDMYAMGLVWELASRCTAADGPVDEYMLPFEEI 422  
 Db 360 RRYMAPEVLEGAINFOADFLRDMYAMGLVWELASRCTAADGPVDEYMLPFEEI 419  
 QY 423 PSLEDQEVVYVHKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCVGERI 482  
 Db 423 PSLEDQEVVYVHKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCVGERI 482

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Db 420 PSLEDQADVAVHKKRPDAFKDCWLKHSGLCOMCETMECDWDHDAEARLSAGCVQERISOI 479
QY 483 ORLNTIITTEDIVTVMVTNVDPPPKESL 513
Db 480 RVSS-STSOCLFSWVTSNLNVDLPKESSI 509
RESULT 9
O13102 PRELIMINARY; PRT; 504 AA.
ID O13102
AC O13102;
DT 01-JUL-1997 (TremBLrel. 04, Created)
DT 01-JUL-1997 (TremBLrel. 04, Last sequence update)
DE 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE Activin type IIB receptor precursor.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN 1
RP SEQUENCE FROM N.A.
PP TISSUE-Ovary.
PP MEDLINE=97424747; PubMed=9278860;
PP Ge W., Tanaka M., Yoshikuni M., Eto Y., Nagahama Y.;
PP "Cloning and characterization of goldfish activin type IIB receptor.";
PP J. Mol. Endocrinol. 19:47-57(1997).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF001406; AAB58749.1;
DR HSPF; P27038; ISTE.
DR InterPro; IPR000472; Activin_rec.
DR InterPro; IPR000333; Actn_receptorII.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF01064; Activin_rec; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00653; ACTIVIN2R.
DR ProDom; PD000001; Euk_pkinase; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Receptor; Serine/threonine-protein kinase; Signal;
KW TRANSFERASE.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 504 ACTIVIN TYPE IIB RECEPTOR.
SQ SEQUENCE 504 AA; 57215 MW; CCB779A07992338F1 CRC64;
Query Match 65.8%; Score 1824; DB 13; Length 504;
Best Local Similarity 64.6%; Pred. No. 8.5e-162;
Matches 329; Conservative 83; Mismatches 81; Indels 16; Gaps 5;
QY 9 FAVFLICSSGAILGRSETQCLFFNANWEKDRNTQGTVEPCYGDKKRRHCFATWKNIS 68
8 FALLIGTFAGSFAEVEHTECLYFNINWEVEKTRNSGVERCEGEKDRSHCYASWRNS 67
QY 69 GSIEVKGCGWLDINCVDYDCVEKDSPEVYFCCGEGNMCEKFSYFFEMEVQPTSN 128
68 GSILVKGCGWLDINCVDYDCVEKDSPEVYFCCGEGNMCEKFSYFFEMEVQPTSN 121
QY 129 PVTPRPYNYNILL----YSLVPLMLIAGIVICAFWYRHHKMYPPVLVPTQDPGPPPS 184
122 PVLESPPSAPLLLIIVLYSLPVTMLSMLLLGFWMYRHRKPPYGHVDL-SEDPSPSPS 180
QY 185 PLLGLKPLQLLEVARGRGFCGWAKQLNVEYVAVKIPFIQDKSQWNEYEYVSLPGMKHE 244
181 PLLTLKPLQLLEVARGRGFCGWAKQLNVEYVAVKIPFIQDKSQWNEYEYVSLPGMKHE 240
QY 245 NTLQFIGAEKRGTSVDVWLITAFHEKGSLSDFLKANNVSNOLCHIAETMARGLAYLH 304
241 NLRIYIGERRGANLETFEFLWITEFHEKGSLSDFLKANNVSNOLCHIAETMARGLAYLH 300
QY 305 EDIPGLKGHKPAISHRDIKSNVLLKNNLTACIADFGALKFEAGKSAGDTHGQVGTTR 364
301 EDVP----RSKPAIAHRDKSNVLLKNNLTACIADFGALKFEAGKSAGDTHGQVGTTR 356

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QY 365 YNAPEVLEGAINFORDAFLRIDMYAMGLVLMELASRCTAADGPDVDEYMLPFEETIGQHP 424
Db 357 YNAPEVLEGAINFORDAFLRIDMYAMGLVLMELASRCTAADGPDVDEYMLPFEETIGQHP 416
QY 425 LEDMQEVVHHKKRPVLRDYQWKHAGMAMLCETIEECWDHDAEARLSAGCVGERITQMOR 484
Db 417 LEDLQADVAVHKKMRPAFKDCWLKHSGLQACMETIEECWDHDAEARLSAGCVGERISQIR 476
QY 485 LFNIIITTEDIVTVMVTNVDPPPKESL 513
Db 477 LHS-ITTSOLLSTVTSNLNVDLSPKESRI 504
RESULT 10
Q9PSG1 PRELIMINARY; PRT; 292 AA.
ID Q9PSG1
AC Q9PSG1;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DE 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE Activin receptor type IIA, ARIIA (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN 1
RP SEQUENCE FROM N.A.
PP MEDLINE=94159615; PubMed=8115385;
PP Nohno T., Noji S., Koyama E., Myokai F., Ohuchi H., Nishikawa K.,
PP Sumitomo S., Taniguchi S., Saito T.;
PP "Expression patterns of the activin receptor IIA and IIB genes during
PP chick limb development.";
PP Prog. Clin. Biol. Res. 383:705-714(1993).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR InterPro; IPR000333; Actn_receptorII.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00653; ACTIVIN2R.
DR ProDom; PD000001; Euk_pkinase; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
FT NON_TER 1
FT NON_TER 292
SQ SEQUENCE 292 AA; 33173 MW; 9486ABDD28A256A1 CRC64;
Query Match 54.2%; Score 1500; DB 13; Length 292;
Best Local Similarity 95.2%; Pred. No. 7.6e-132;
Matches 278; Conservative 11; Mismatches 3; Indels 0; Gaps 0;
QY 194 LLEVKARGFGCVKQAQLNVEYVAVKIPFIQDKSQWNEYEYVSLPGMKHNILOFIGAE 253
Db 1 LLEIKARGFGCVKQAQLNVEYVAVKIPFIQDKSQWNEYEYVSLPGMKHNILOFIGAE 60
QY 254 KRCTSDVDLWLITAFHEKGSLSDFLKANNVSNOLCHIAETMARGLAYLHEDIFGLKDG 313
Db 61 KRCTSDVDLWLITAFHEKGSLSDFLKANNVSNOLCHIAETMARGLAYLHEDIFGLKDG 120
QY 314 HKPAISHRDIKSNVLLKNNLTACIADFGALKFEAGKSAGDTHGQVGTTRRYMAPEVLEG 373
Db 121 HKPAISHRDIKSNVLLKNNLTACIADFGALKFEAGKSAGDTHGQVGTTRRYMAPEVLEG 180
QY 374 AINFQDAFLRIDMYAMGLVLMELASRCTAADGPDVDEYMLPFEETIGQHPSEDMQEVVV 433
Db 181 AINFQDAFLRIDMYAMGLVLMELASRCTAADGPDVDEYMLPFEETIGQHPSEDMQEVVV 240
QY 434 HKKRPVLRDYQWKHAGMAMLCETIEECWDHDAEARLSAGCVGERITQMORL 485

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Db 241 HKKKRPVLRCEWQKHSGMAMLCETIEECWDHDAEARLSAGCVEERIOMOKL 292

RESULT 11

|        |   |      |         |
|--------|---|------|---------|
| Q91347 | PRELIMINARY;  | PRT; | 365 AA. |
| ID     |   |      |         |
| AC     | Q91347;   |      |         |
| DT     | 01-NOV-1996 (TrEMBLrel. 01, Created)                                |      |         |
| DT     | 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)                   |      |         |
| DT     | 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)                 |      |         |
| DE     | Activin receptor.   |      |         |
| DE     |   |      |         |
| GN     | XSTK2.  |      |         |
| OS     | Xenopus laevis (African clawed frog).                               |      |         |
| OS     | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   |      |         |
| OC     | Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;       |      |         |
| OC     | Xenopodinae; Xenopus.   |      |         |
| OX     | NCBI_TaxID=8355;  |      |         |
| OX     | [1]   |      |         |
| RP     | SEQUENCE FROM N.A.  |      |         |
| RX     | MEDLINE=93050187; PubMed=1330691;                                   |      |         |
| RX     | Nishimatsu S., Iwao M., Nagai T., Oda S., Suzuki A., Asashima M.,   |      |         |
| RT     | Murakami K., Ueno N.;   |      |         |
| RT     | "A carboxyl-terminal truncated version of the activin receptor      |      |         |
| RL     | mediates activin signals in early Xenopus embryos.";                |      |         |
| RL     | FEBS Lett. 312:169-173(1992).                                       |      |         |
| CC     | -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.   |      |         |
| CC     | EMBL: S47891; AAB24030.1; -;  |      |         |
| DR     | HSSP; P27038; 1BTE.   |      |         |
| DR     | InterPro: IPR000472; Activin_rec.                                   |      |         |
| DR     | InterPro: IPR000719; Euk_pkinase.                                   |      |         |
| DR     | InterPro: IPR002290; Ser_thr_pkinase.                               |      |         |
| DR     | Pfam: PF01064; Activin_recip; 1.                                    |      |         |
| DR     | Pfam: PF00069; pkinase; 1.  |      |         |
| DR     | ProDom: PD000001; Euk_pkinase; 1.                                   |      |         |
| DR     | PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.                            |      |         |
| DR     | PROSITE: PS00108; PROTEIN_KINASE_ST; 1.                             |      |         |
| KW     | ATP-binding; Receptor; Serine/threonine-protein kinase; Transferase |      |         |
| SK     | SEQUENCE 365 AA; 41401 MW; 36EFC50EE7CE616 CRC64;                   |      |         |

Query Match 47.4%; Score 1312.5; DB 13; Length 365;  
Best Local Similarity 62.5%; Pred. No. 3.7e-114;  
Matches 227; Conservative 72; Mismatches 59; Indels 5; Gaps 3;

|    |     |     |   |   |   |   |   |   |   |   |   |    |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |    |   |   |   |    |     |   |     |   |   |   |   |     |
|----|-----|-----|---|---|---|---|---|---|---|---|---|----|----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|----|---|---|---|----|-----|---|-----|---|---|---|---|-----|
| QY | 1   | MGA | A | A | F | A | F | V | L | L | S | C  | S  | G | A | I | L | G | R | S | T | O | E | C | L | F | F | N | A | N | E | K | D | R | I | N | O | T | G | V | E | P | C | Y | G | D | K | R  | R | H | C | 60 |     |   |     |   |   |   |   |     |
|    |     |     |   |   |   |   |   |   |   |   |   |    |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |    |   |   |   |    |     |   |     |   |   |   |   |     |
|    |     |     |   |   |   |   |   |   |   |   |   |    |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |    |   |   |   |    |     |   |     |   |   |   |   |     |
|    |     |     |   |   |   |   |   |   |   |   |   |    |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |    |   |   |   |    |     |   |     |   |   |   |   |     |
| QY | 61  | F   | A | T | W | K | N | I | S | G | S | E  | I  | V | K | O | G | C | L | D | D | I | N | C | V | D | R | T | D | C | V | E | K | D | S | P | E | V | F | C | C | B | G | N | C | N | E | K  | F | S | F | P  | P   | M | 120 |   |   |   |   |     |
|    |     |     |   |   |   |   |   |   |   |   |   |    |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |    |   |   |   |    |     |   |     |   |   |   |   |     |
| DB | 61  | Y   | A | S | W | R | N | N | S | G | F | E  | I  | V | K | G | C | L | D | D | F | N | C | V | D | R | O | E | T | A | K | E | N | P | O | V | F | C | C | B | G | N | C | N | K | F | T | H  | L | P | E | V  | 120 |   |     |   |   |   |   |     |
|    |     |     |   |   |   |   |   |   |   |   |   |    |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |    |   |   |   |    |     |   |     |   |   |   |   |     |
| QY | 121 | E   | V | T | O | P | T | S | N | P | T | P  | P  | P | P | P | N | I | L | L | S | L | V | L | P | L | M | L | I | A | G | I | V | I | C | A | F | W | Y | R | H | K | W | A | Y | P | V | L  | P | T | O | D  | C   | P | 180 |   |   |   |   |     |
|    |     |     |   |   |   |   |   |   |   |   |   |    |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |    |   |   |   |    |     |   |     |   |   |   |   |     |
| DB | 121 | E   | T | E | D | P | R | P | O | P | M | -- | -- | P | S | V | N | I | L | I | S | L | L | P | I | A | G | L | S | W | L | I | A | F | W | Y | R | H | R | K | P | P | Y | G | H | V | D | -- | N | E | D | P  | 176 |   |     |   |   |   |   |     |
| QY | 181 | P   | P | S | P | L | G | L | K | P | L | L  | E  | K | A | R | G | R | G | C | V | W | K | A | Q | L | L | N | E | Y | V | A | K | I | F | I | P | T | O | D | K | S | Q | W | N | E | Y | E  | V | S | L | P  | 240 |   |     |   |   |   |   |     |
|    |     |     |   |   |   |   |   |   |   |   |   |    |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |    |   |   |   |    |     |   |     |   |   |   |   |     |
| DB | 177 | S   | P | S | P | M | V | G | L | K | P | L  | L  | E | K | A | R | G | R | G | C | V | W | K | A | Q | L | L | N | E | Y | V | A | K | I | F | P | V | O | D | K | S | Q | W | C | E | K | E  | I | N | T | P  | 236 |   |     |   |   |   |   |     |
| QY | 241 | M   | K | H | E | N | I | L | O | F | T | G  | A  | E | K | R | G | T | S | V | D | V | L | W | L | I | T | A | F | H | E | K | G | S | L | S | D | F | L | K | A | N | V | V | S | N | O | L  | C | H | I | A  | E   | T | M   | A | R | G | L | 300 |
|    |     |     |   |   |   |   |   |   |   |   |   |    |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |    |   |   |   |    |     |   |     |   |   |   |   |     |
| DB | 237 | M   | K | H | E | N | L | E | F | T | A | A  | E  | K | R | G | N | I |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |    |   |   |   |    |     |   |     |   |   |   |   |     |

Qy 360 VGT 362

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RESULT 12

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Q9PSL7
ID Q9PSL7 PRELIMINARY; PRT; 386 AA.
AC Q9PSL7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE ACTIVIN RECEPTOR-CLONE XSTR2.
DS
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC xenopodinae; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92275088; PubMed=1317302;
RA Nishimatsu S., Oda S., Murakami K., Ueno N.;
RT "Multiple genes for Xenopus activin receptor expressed during early
  embryogenesis.";
RL FEBS Lett. 303:81-84(1992).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR HSP: P27038; 1BTE.
DR InterPro: IPR000472; Activin_rec.
DR InterPro: IPR000333; Actn_receptorII.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF01064; Activin_rec; 1.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00653; ACTIVIN2R.
DR ProDom: PD000001; Euk_pkinase; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding: Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 386 AA; 43719 MW; 559F3F51AE4419CC CRC64;

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|                       |              |                   |                |             |
|-----------------------|--------------|-------------------|----------------|-------------|
| Query Match           | 47.4%        | Score 1312.5;     | DB 13;         | Length 386; |
| Best Local Similarity | 62.5%;       | Pred. No. 4e-114; |                |             |
| Matches 227;          | Conservative | 72;               | Mismatches 59; | Indels 5;   |
|                       |              |                   |                | Gaps 3;     |

[illegible]

RESULT 13

|                |                                       |      |         |
|----------------|---------------------------------------|------|---------|
| Q24468         | PRELIMINARY;                          | PRT; | 516 AA. |
| ID Q24468      |                                       |      |         |
| AC Q24468;     |                                       |      |         |
| DT 01-NOV-1996 | (TREMBlrel. 01, Created)              |      |         |
| DT 01-NOV-1996 | (TREMBlrel. 01, Last sequence update) |      |         |

01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 PUT OR PUNT OR CG7904.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., D.L.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Fang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster";  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=95211840; PubMed=7697719;  
 RA Basler K.;  
 RT "An absolute requirement for both the type II and type I receptors,  
 RT punt and thick veins, for dpp signaling in vivo";  
 RL Cell 80:889-897(1995).  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR ENBL; AE003705; AACF5079.1; -;  
 DR ENBL; L38495; AAC41566.1; -;  
 DR FlyBase; FBgn0003169; put.  
 DR InterPro; IPR000472; Activin\_rec.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR Pfam; PF01064; Activin\_rec; 1.  
 DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000001; Euk\_pkinase; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 516 AA; 58648 MW; B3F754DC603EC5BC CRC64;

Query Match

41.5%; Score 1150.5; DB 5; Length 516;

Best Local Similarity 47.2%; Pred. No. 8.9e-99;  
 Matches 249; Conservative 83; Mismatches 152; Indels 43; Gaps 17;  
 QY 5 AKLAFAVFLSCSGAILGRSETQCLFFNANWEK--DRTNQ--TGVEPCYGDKKRRHC 60  
 DB 11 AQLTIVCLLIGHGSLPGSHGIECEHFD---EKMCNTTOCETRIEHCWEADKPPSC 67  
 QY 61 FATW--KNISGSIEIVKOGCWLDDINCYDRDTCVCKKDSPE--VYFCCCEGNCNEKFSY 116  
 DB 68 YVLWSVNETTILRIKMGCEFTDMHEC--NOTECVTSABEQGNIHFCCKGSRCSNQY 126  
 QY 117 FPE-----MEVTOPTSNPVTPEPKPYNYLLSLVPLMLIAGIVICAFWVYRHHKMA 167  
 DB 127 IKSTTEATQVPKERTQGSNLIY---IYIGTSVFSV--LMVIYGM---GLLLRRRQKA 178  
 QY 168 YPVLVLPVTPQDPPPPPLGLKPLQLLEVKARGFCVWKAQLLNEYVAYKFIPIODQK 227  
 DB 179 HENE-IPTHEAETITNSPLLSNRPIQLLEQKASRGFDGVQWQAKLNQDVAVKIFRMQKE 237  
 QY 228 SQNQEYVSLPGMKHENILOFIGAERKGTVD--VDMLITAFHEKSGSLDFLKNVYSW 286  
 DB 238 SWTTEHDIVKLPFRMRPNLLEFLGVKEH---MDKPEYWLISYQHNGSLCDYLKSHSTISW 294  
 QY 287 NOLCHIAETMARGLAYLHEDIPGLK-DGHPAISHRDITKSNVLLKNLTACIADFGLAL 345  
 DB 295 PELCRIAESMANGLAHLHEEIPASKTDLKPSIAHRDFKSNVLLKSLDTACIADFGLAM 354  
 QY 346 KFEAGKSGADTHGQVGTTRYMAPEVLEGAINFQRFDAFLRIDMYAMGLVWLWELASRCTAAD 405  
 DB 355 IFQPKPCGDTHGQVGTTRYMAPEVLEGAINFNRDAFLRIDVYACGLVWELWMSRCDFA- 413  
 QY 406 GPVDEYMLPFEEICQHPLESLEDMQEVVYHKRPVLRDYWKQKHAGMAMLCETIECDWDHD 465  
 DB 414 GVGVEFQLPFEEALGLRPSLDEVQESVYVYMKLRLPRLLSNRAHPLGNLFCDTMECDWDHD 473  
 QY 466 AEARLSAGCVGERITQMORLTNIITTEDIVTVMTVMTVDPKPKSS 512  
 DB 474 AEARLSGCVMERFAQLNKYPS-----TQLLKNTNID-DAKEST 513  
 RESULT 14  
 ID Q24229 PRELIMINARY; PRT; 516 AA.  
 AC Q24229;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DT Activin receptor.  
 GN PUT OR CG7904.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94022397; PubMed=8415726;  
 RA Childs S.R., Wrana J.L., Arora K., Attisano L., O'Connor M.B.,  
 RA Massague J.;  
 RT "Identification of a Drosophila activin receptor";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:9475-9479(1993).  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; L22176; AAA03579.1; -;  
 DR FlyBase; FBgn0003169; put.  
 DR InterPro; IPR000472; Activin\_rec.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF01064; Activin\_rec; 1.  
 DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000001; Euk\_pkinase; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Serine/threonine-protein kinase; Transferase.

SQ SEQUENCE 516 AA; 58643 MW; 3C3B2DDC603EC5BB CRC64;

Query Match 41.4%; Score 1147.5; DB 5; Length 516;  
Best Local Similarity 47.8%; Pred. No. 1.7e-98;  
Matches 251; Conservative 83; Mismatches 144; Indels 47; Gaps 19;

QY 11 VFLISC---SSGAIL-GRSETOCELFNFANWEK--DRTNQ--TGVEPCVGDKDKRRHCF 62  
DB 13 VTLVCLLIGHGSLPGSHGIIIECHFD--EKMCNTQQCEFHCKMEADKFPSCYV 69  
QY 63 TW--KNISGIEIVKOGCWLDDINCYDRDCVEKKDSPE--VYFCCCGNMCNEKFSYFP 118  
DB 70 LMSVNETTGILRIKMKGCFTDHEC--NOTECVTSAPROGNIHFCCCKSRCNSNQKVIK 128  
QY 119 E-----MEVTOPTSPNVPKPPYYNLLYSVLPLMLIAGIYCAFWYRHHKMAYP 169  
DB 129 STEATTVQPKETQDGSNLIY---IYIGTSVFSV--LMVIVGM--GLLLYRRRKQAHF 180  
QY 170 PVLVPTQDPGPPPPSLGLKPLQLLEVKARGFCVKAQLLNEYVAVKIPPIQDKQSW 229  
DB 181 NE-IPTHEAEITNSSPLLSNRPIQLLEOKASGRFGDVQWAKLNNOVDVAVKIFRQEKESW 239  
QY 230 QNEYEYVSLPGMKHENILOFIGAERKTSVD--VDLWLITAFHEKSLSDFLKANVVSQW 288  
DB 240 TTEHDIYKLPWRHPNILEFLGVERH--MDKPEYWLITSTYOHNGSLCDYLKSHTSWPE 296  
QY 289 LCHIAETMARGLAYLHEDIPGLK-DGHKPAISHRDIKSNVLLKNLTACTADFGALKF 347  
DB 297 LCRIAESMANGLAHLHEEIPASKTDLKPSIAHRDFKSNVLLKSDLTACTADFGALMIF 356  
QY 348 EAGKSGDTHGVGTRRYMAPEVLEGAINFORDAFLRIDMYAMGLVLMELASRCTAADGP 407  
DB 357 QPGKPCGDPHGVGTRRYMAPEVLEGAINFORDAFLRIDMYAMGLVLMELASRCTAADGP 415  
QY 408 VDEYMLPREEEIGQHPSLDEQVYVHKRPVLRDYQKQKAGMAMLCETIEECWDHDAE 467  
DB 416 VGEFQLPFAELGLRPSLDEQVYVHKRPVLRDYQKQKAGMAMLCETIEECWDHDAE 475  
QY 468 ARLSAGCGERITQORLTNIITTEDIVTVMTNVDFFPKPKESS 512  
DB 476 ARLSSSCVMERFAQLNKYPS-----TQLLKNHTNID-DAKEST 513

RESULT 15

P79233 PRELIMINARY; PRT; 254 AA.  
DT 01-MAY-1997 (TRENBLrel. 03, Created)  
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)  
DT 01-MAY-2002 (TRENBLrel. 20, Last annotation update)  
DE Activin receptor-like kinase (Fragment).  
OS Papio hamadryas (Hamadryas baboon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Papio.  
OX NCBI\_taxid=9557;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LUNG;  
RX MEDLINE=97112402; PubMed=8954082;  
RA Zhao Y., Silbajoris R., Young S.L.;  
RT "Identification and developmental expression of two activin receptors  
in baboon lung.";  
RL Biochem. Biophys. Res. Commun. 229:50-57(1996).  
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR EMBL: U60421; AAB40074.1; -  
DR InterPro; IPR000719; Euk\_pkinase.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00069; pkinase; 1.  
DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD000001; Euk\_pkinase; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW Kinase; Receptor; Serine/threonine-protein kinase.  
FT NON\_TER 1  
FT NON\_TER 254  
SQ SEQUENCE 254 AA; 29041 MW; 481912040C3DC7DA CRC64;  
Query Match 38.7%; Score 1071; DB 6; Length 254;  
Best Local Similarity 75.2%; Pred. No. 8.4e-92;  
Matches 191; Conservative 38; Mismatches 21; Indels 4; Gaps 2;  
QY 216 VAVKIFPIQDKQSWQNEVEYVSLPGMKHENILOFIGAERKTSVDVLDLWLTAFHEKGS 275  
DB 1 VAVKIFPIQDKQSWQNEVEYVSLPGMKHENILOFIGAERKTSVDVLDLWLTAFHEKGS 60  
QY 276 SDFLKANVVSQWNLCHIAETMARGLAYLHEDIPGLK-DGHKPAISHRDIKSNVLLKNL 334  
DB 61 TDYLGKNIITWNECHVAETMSRGLSLHVEVPWCRGEGHKPSIAHRDFKSNVLLKSDL 120  
QY 335 ---TACIADFGALKEFGKSGAGDTHGVGTRRYMAPEVLEGAINFORDAFLRIDMYAMG 391  
DB 121 ILTAVLADFGALKEFGKSGAGDTHGVGTRRYMAPEVLEGAINFORDAFLRIDMYAMG 180  
QY 392 LVLWELASRCTAADGPVDEYMLPREEEIGQHPSLDEQVYVHKRPVLRDYQKQKAGM 451  
DB 181 LVLWELVSRSKAADGPVDEYMLPREEEIGQHPSLDEQVYVHKRPVLRDYQKQKAGM 240  
QY 452 AMLCETIEECWDHD 465  
DB 241 AQLCVTIEECWDHD 254

Search completed: May 10, 2003, 18:08:47  
Job time : 94 secs



GenCore version 5.1.4.p5\_4578  
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OM protein - protein search, using sw model

Run on: May 10, 2003, 17:59:50 ; Search time 27 Seconds  
(without alignments)  
788.050 Million cell updates/sec

Title: US-09-742-684A-16

Perfect score: 2770

Sequence: 1 MGAALKAFAPFLISCSGA.....IVTVTMTNVDFPPKSSL 513

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score  | Query Match % | Length | ID | Description |
|------------|--------|---------------|--------|----|-------------|
| 1          | 2767   | 99.9          | 513    | 1  | AVR2_HUMAN  |
| 2          | 2763   | 99.7          | 513    | 1  | AVR2_MOUSE  |
| 3          | 2750   | 99.3          | 513    | 1  | AVR2_RAT    |
| 4          | 2743   | 99.0          | 513    | 1  | AVR2_BOVIN  |
| 5          | 2704   | 97.6          | 513    | 1  | AVR2_SHEEP  |
| 6          | 2482.5 | 89.6          | 514    | 1  | AVR2_XENLA  |
| 7          | 1947   | 70.3          | 511    | 1  | AVRB_XENLA  |
| 8          | 1844   | 70.2          | 512    | 1  | AVRB_HUMAN  |
| 9          | 1937   | 69.9          | 512    | 1  | AVRB_BOVIN  |
| 10         | 1934   | 69.8          | 536    | 1  | AVRB_MOUSE  |
| 11         | 1460   | 52.7          | 382    | 1  | AVRB_RAT    |
| 12         | 779    | 28.1          | 592    | 1  | TGR2_MOUSE  |
| 13         | 777.5  | 28.1          | 567    | 1  | TGR2_RAT    |
| 14         | 775.5  | 28.0          | 567    | 1  | TGR2_HUMAN  |
| 15         | 775.5  | 28.0          | 1038   | 1  | BMR2_HUMAN  |
| 16         | 770.5  | 27.8          | 1038   | 1  | BMR2_MOUSE  |
| 17         | 674    | 24.3          | 532    | 1  | BMRA_HUMAN  |
| 18         | 669    | 24.2          | 532    | 1  | BMRA_MOUSE  |
| 19         | 653.5  | 23.6          | 502    | 1  | BMRB_HUMAN  |
| 20         | 647.5  | 23.4          | 502    | 1  | BMRB_MOUSE  |
| 21         | 624.5  | 22.5          | 502    | 1  | BMRB_CHICK  |
| 22         | 624    | 22.5          | 501    | 1  | TGR1_RAT    |
| 23         | 624    | 22.5          | 503    | 1  | TGR1_HUMAN  |
| 24         | 622.5  | 22.5          | 503    | 1  | TGR1_MOUSE  |
| 25         | 613.5  | 22.1          | 505    | 1  | KIR2_HUMAN  |
| 26         | 611.5  | 22.1          | 505    | 1  | KIR2_RAT    |
| 27         | 587.5  | 21.2          | 509    | 1  | AVR1_HUMAN  |
| 28         | 586    | 21.2          | 509    | 1  | AVR1_BOVIN  |
| 29         | 582    | 21.0          | 509    | 1  | AVR1_MOUSE  |
| 30         | 582    | 21.0          | 744    | 1  | DAF4_CAEEL  |
| 31         | 576    | 20.8          | 503    | 1  | KIR3_HUMAN  |
| 32         | 575.5  | 20.8          | 503    | 1  | AVR1_RAT    |
| 33         | 559    | 20.2          | 573    | 1  | AMH2_HUMAN  |

34 553.5 20.0 505 1 KIR3\_RAT  
35 551 19.9 502 1 KIR3\_MOUSE  
36 531 19.2 557 1 AMH2\_RAT  
37 517 18.7 669 1 DAF1\_CAEEL  
38 465.5 16.8 636 1 SMA6\_CAEEL  
39 291.5 10.5 518 1 RIK3\_HUMAN  
40 279.5 10.1 486 1 RIK3\_MOUSE  
41 279 10.1 478 1 RIK3\_RAT  
42 272.5 9.8 1584 1 KYK1\_DICDI  
43 263.5 9.5 393 1 M3K7\_DROME  
44 240.5 8.7 821 1 CTRL\_ARATH  
45 235.5 8.5 849 1 SRK6\_BRAOL

P80203 rattus norv  
Q61288 mus musculu  
Q62893 rattus norv  
P20792 caenorhabdi  
Q09488 caenorhabdi  
Q9Y572 homo sapien  
Q9Q210 mus musculu  
Q9Z2P5 rattus norv  
P18160 dictyosteli  
P83104 drosophila  
Q05609 arabidopsis  
Q09092 brassica ol

## ALIGNMENTS

### RESULT 1

AVR2\_HUMAN STANDARD; PRT; 513 AA.  
AC P27037; Q92474;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Activin receptor type II precursor (EC 2.7.1.37) (ACTR-II) (ACTRIA).  
GN ACVR2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
TISSUE=Testis;  
RX MEDLINE=92182002; PubMed=13111955;  
RA Matzuk M.M., Bradley A.;  
RT "Cloning of the human activin receptor cDNA reveals high evolutionary conservation.";  
RL Biochim. Biophys. Acta 1130:105-108(1992).  
[2]  
SEQUENCE FROM N.A.  
TISSUE=Testis;  
RX MEDLINE=92231944; PubMed=1314589;  
RA Donaldson C.J., Mathews L.S., Vale W.W.;  
RT "Molecular cloning and binding properties of the human type II activin receptor.";  
RL Biochem. Biophys. Res. Commun. 184:310-316(1992).  
[3]  
SEQUENCE FROM N.A.  
TISSUE=Mammary gland;  
RA Geiser A.G.;  
RL Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.  
[4]  
SEQUENCE FROM N.A.  
RA Iimura T., Oida S.;  
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.  
CC -|- FUNCTION: RECEPTOR FOR ACTIVIN A, ACTIVIN B, AND INHIBIN A.  
CC -|- INVOLVED IN TRANSMEMBRANE SIGNALING.  
CC -|- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.  
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC TGFBR RECEPTOR SUBFAMILY.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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DR EMBL; X63128; CAA44839.1; -;  
DR EMBL; X62381; CAA44245.1; -;  
DR EMBL; M93415; AAA35504.1; -;

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EMBL; D31770; BAA06548.1; -.
DR PIR; S18908; S18908.
DR PIR; JQ1486; JQ1486.
DR PIR; S22345; S22345.
DR HSP; P27038; ISTE..
DR Genew; HGNC:173; ACVR2.
DR MM; 102581; -.
DR InterPro; IPR000472; Activin_rec.
DR InterPro; IPR000333; Actn_receptorII.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF01064; Activin_rec; 1.
DR PRINTS; PR00653; ACTIVIN2R.
DR PRODOM; PD000001; Euk_pkinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 513
FT DOMAIN 20 135
FT TRANSMEM 136 161
FT DOMAIN 162 513
FT NP_BIND 198 206
FT BINDING 219 219
FT ACT_SITE 322 322
FT CARBOHYD 43 43
FT CARBOHYD 66 66
FT CONFLICT 13 13
FT CONFLICT 204 206
FT CONFLICT 348 348
SQ SEQUENCE 513 AA; 57847 MW; A89822E880979618 CRC64;

Query Match 99.98; Score 2767; DB 1; Length 513;
Best Local Similarity 99.88; Pred. No. 2e-199;
Matches 512; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MGAAKLAFVFLSCSGAILGRSETQECLEFFNANNEKDRNTGTGVCYGDKRRHC 60
Db 1 MGAAKLAFVFLSCSGAILGRSETQECLEFFNANNEKDRNTGTGVCYGDKRRHC 60
Oy 61 FATWNISGSIEIVKQGCWLDINDCYDRTDCVEKKDSPEVYFCCCEGNCNEKFSYPPEM 120
Db 61 FATWNISGSIEIVKQGCWLDINDCYDRTDCVEKKDSPEVYFCCCEGNCNEKFSYPPEM 120
Oy 121 EVTQPTSNPVTPKPPYYNILLVSLVPLMLIAGIVICAFWYRHHKMAYPVLYVPTQDGP 180
Db 121 EVTQPTSNPVTPKPPYYNILLVSLVPLMLIAGIVICAFWYRHHKMAYPVLYVPTQDGP 180
Db 181 PPPSLGLKPLQLLEVKARGFCVCKAQLNLLNEYVAVKIPFIQDKGSQWNEYEVYSLPG 240
Db 181 PPPSLGLKPLQLLEVKARGFCVCKAQLNLLNEYVAVKIPFIQDKGSQWNEYEVYSLPG 240
Oy 241 MKHENILOFIGAERKGTSDVDLMLITAFHEKGSLSDFLKNVYVSNQOLCHIAETMARGL 300
Db 241 MKHENILOFIGAERKGTSDVDLMLITAFHEKGSLSDFLKNVYVSNQOLCHIAETMARGL 300
Oy 301 AYLHEDIPGLKDGHPALSHRDIKSNVLLKNLITACTADPGLALKEFGKSGAGDTHGOV 360
Db 301 AYLHEDIPGLKDGHPALSHRDIKSNVLLKNLITACTADPGLALKEFGKSGAGDTHGOV 360
Oy 361 GTRRYMAPEVLEGAINFORDAFRLIDRYAMGLVLWELASRCAADGPVDEYMLPFEEIG 420
Db 361 GTRRYMAPEVLEGAINFORDAFRLIDRYAMGLVLWELASRCAADGPVDEYMLPFEEIG 420
Oy 421 QHPSLEDQEVVVVHKKRPVLRDQWQKHAGNMLCETIEECWDHDAEARLSAGCVGRIT 480
Db 421 QHPSLEDQEVVVVHKKRPVLRDQWQKHAGNMLCETIEECWDHDAEARLSAGCVGRIT 480
Oy 481 QMQLRTNIITTTDIVVTVMVTNVDFFPKSSSL 513

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Db 481 QMQLRTNIITTTDIVVTVMVTNVDFFPKSSSL 513
RESULT 2
AVR2_MOUSE
ID AVR2_MOUSE STANDARD; PRT; 513 AA.
AC P27038;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Activin receptor type II precursor (EC 2.7.1.37) (ACTR-II).
GN ACVR2 OR ACVR2A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91256317; PubMed=1646080;
RA Mathews L.S., Vale W.W.;
RT "Expression cloning of an activin receptor, a predicted transmembrane
serine kinase.";
RL Cell 65:973-982(1991).
RN [2]
RX X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 25-121.
RX MEDLINE=99101377; PubMed=9886286;
RA Greenwald J., Fischer W.H., Vale W.W., Choe S.;
RT "Three-finger toxin fold for the extracellular ligand-binding domain
of the type II activin receptor serine kinase.";
RL Nat. Struct. Biol. 6:18-22(1999).
CC -!- FUNCTION: RECEPTOR FOR ACTIVIN A, ACTIVIN B, AND INHIBIN A.
CC -!- INVOLVED IN TRANSMEMBRANE SIGNALING.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: BRAIN, TESTIS, INTESTINE, LIVER, AND KIDNEY.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
TGFB RECEPTOR SUBFAMILY.
-----
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or send an email to license@isb-sib.ch).
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EMBL; M65287; AAA37171.1; -.
DR PIR; A39896; A39896.
DR PDB; 1BTE; 09-FEB-99.
DR MGD; MGI:102806; Acvr2.
DR InterPro; IPR000472; Activin_rec.
DR InterPro; IPR000333; Actn_receptorII.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF01064; Activin_rec; 1.
DR PRINTS; PR00653; ACTIVIN2R.
DR PRODOM; PD000001; Euk_pkinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Transmembrane; Glycoprotein; Signal; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 513
FT DOMAIN 20 135
FT TRANSMEM 136 161
FT DOMAIN 162 513
FT NP_BIND 198 206
FT BINDING 219 219
FT ACT_SITE 322 322

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FT CARBOHYD 43 43 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 66 66 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 513 AA; 57889 MW; 475CD292506BAC61 CRC64;

Query Match 99.7%; Score 2763; DB 1; Length 513;
Best Local Similarity 99.4%; Pred. No. 3.9e-199;
Matches 510; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAALAFVFLISCGSAILGRSETQCLFFNANWEKDRNTQGTVEPCYGDKDKRRHC 60
DQ 1 MGAALAFVFLISCGSAILGRSETQCLFFNANWEKDRNTQGTVEPCYGDKDKRRHC 60
QY 61 FATWKNISGSIEIVKOGCWLDDINCVDYRDCVEKDKSPVYFCCCGNMCNEKESYFPEM 120
DQ 61 FATWKNISGSIEIVKOGCWLDDINCVDYRDCVEKDKSPVYFCCCGNMCNEKESYFPEM 120
QY 121 EVTQPTSNPVTPKPPYNNILLYSLVPLMLIAGIVICAFWYVRHHKWAYPPVLVPTQDPGP 180
DQ 121 EVTQPTSNPVTPKPPYNNILLYSLVPLMLIAGIVICAFWYVRHHKWAYPPVLVPTQDPGP 180
QY 181 PPPSPLLGKPLQLLEVKARGGCVWKAQLLNEYVAVKIFPIQDKOSQWNEVEVYSLPG 240
DQ 181 PPPSPLLGKPLQLLEVKARGGCVWKAQLLNEYVAVKIFPIQDKOSQWNEVEVYSLPG 240
QY 241 MKHENILQFTGAERKGTSDVDLMLITAFHEKGSLSDFLKANVYSWNLCHIAETMARGL 300
DQ 241 MKHENILQFTGAERKGTSDVDLMLITAFHEKGSLSDFLKANVYSWNLCHIAETMARGL 300
QY 301 AYLHEDIPGLKDGKHPAISHRDIKSNVLLKNNLTACIADFGALKEAGKAGDTHGOV 360
DQ 301 AYLHEDIPGLKDGKHPAISHRDIKSNVLLKNNLTACIADFGALKEAGKAGDTHGOV 360
QY 361 GTRRYMAPEVLEGAINFQDAFLRIDMYAMGLVWELASRCCTAAGDPVDEYMLPFEETG 420
DQ 361 GTRRYMAPEVLEGAINFQDAFLRIDMYAMGLVWELASRCCTAAGDPVDEYMLPFEETG 420
QY 421 QHPSLEDMQEVVVKHKKRPVLDYQKDHAGMAMLCETIEECWDHDAEARSAGCGERIT 480
DQ 421 QHPSLEDMQEVVVKHKKRPVLDYQKDHAGMAMLCETIEECWDHDAEARSAGCGERIT 480
QY 481 QMORLTNIITTEDIVVTWTVNVDPPKRESSL 513
DQ 481 QMORLTNIITTEDIVVTWTVNVDPPKRESSL 513

RESULT 3
AVR2_RAT STANDARD; PRT; 513 AA.
ID AVR2_RAT
AC P38444;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Activin receptor type II precursor (EC 2.7.1.37) (ACTR-II).
GN ACVR2 OR ACTRII.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Testis;
RX MEDLINE=93279247; PubMed=7916681;
RA Feng Z.M., Madigan M.B., Chen C.L.C.;
RT "Expression of type II activin receptor genes in the male and female
RL reproductive tissues of the rat.";
RN Endocrinology 132:2593-2600(1993).
RP [2]
RC SEQUENCE FROM N.A.
RX TISSUE=Ovary;
RA MEDLINE=93050162; PubMed=1385212;
RA Shinozaki H., Ito I., Hasegawa Y., Nakamura K., Igarashi S.,
RA Nakamura M., Miyamoto K., Eto Y., Ibuki Y., Minegishi T.;
RT "Cloning and sequencing of a rat type II activin receptor.";
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RL FEBS Lett. 312:53-56(1992).
CC -!- FUNCTION: RECEPTOR FOR ACTIVIN A, ACTIVIN B, AND INHIBIN A.
CC INVOLVED IN TRANSMEMBRANE SIGNALING.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC TGFB RECEPTOR SUBFAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L10639; AAA40674.1; -;
CC EMBL; S48190; AAB23958.1; -;
CC HSSP; P27038; 1BTE.
CC InterPro; IPR000472; Activin_rec.
CC InterPro; IPR000333; Actn_receptorII.
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; pkinase; 1.
CC PRINTS; PR01064; Activin_rec; 1.
CC PRINTS; PR00653; ACTIVIN2R.
CC ProDom; PD000001; Euk_pkinase; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 513 ACTIVIN RECEPTOR TYPE II.
FT DOMAIN 20 135 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 136 161 POTENTIAL.
FT DOMAIN 162 513 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 192 485 PROTEIN KINASE.
FT NP_BIND 198 206 ATP (BY SIMILARITY).
FT BINDING 219 219 ATP (BY SIMILARITY).
FT ACT_SITE 322 322 BY SIMILARITY.
FT CARBOHYD 43 43 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 66 66 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 165 165 M -> K (IN REF. 2).
FT CONFLICT 218 218 V -> I (IN REF. 2).
FT CONFLICT 353 353 G -> A (IN REF. 2).
FT CONFLICT 475 475 L -> V (IN REF. 2).
SQ SEQUENCE 513 AA; 57892 MW; CE3A8742EF91DD7D CRC64;

Query Match 99.3%; Score 2750; DB 1; Length 513;
Best Local Similarity 98.8%; Pred. No. 3.7e-198;
Matches 507; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGAALAFVFLISCGSAILGRSETQCLFFNANWEKDRNTQGTVEPCYGDKDKRRHC 60
DQ 1 MGAALAFVFLISCGSAILGRSETQCLFFNANWEKDRNTQGTVEPCYGDKDKRRHC 60
QY 61 FATWKNISGSIEIVKOGCWLDDINCVDYRDCVEKDKSPVYFCCCGNMCNEKESYFPEM 120
DQ 61 FATWKNISGSIEIVKOGCWLDDINCVDYRDCVEKDKSPVYFCCCGNMCNEKESYFPEM 120
QY 121 EVTQPTSNPVTPKPPYNNILLYSLVPLMLIAGIVICAFWYVRHHKWAYPPVLVPTQDPGP 180
DQ 121 EVTQPTSNPVTPKPPYNNILLYSLVPLMLIAGIVICAFWYVRHHKWAYPPVLVPTQDPGP 180
QY 181 PPPSPLLGKPLQLLEVKARGGCVWKAQLLNEYVAVKIFPIQDKOSQWNEVEVYSLPG 240
DQ 181 PPPSPLLGKPLQLLEVKARGGCVWKAQLLNEYVAVKIFPIQDKOSQWNEVEVYSLPG 240
QY 241 MKHENILQFTGAERKGTSDVDLMLITAFHEKGSLSDFLKANVYSWNLCHIAETMARGL 300
DQ 241 MKHENILQFTGAERKGTSDVDLMLITAFHEKGSLSDFLKANVYSWNLCHIAETMARGL 300
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Qy 301 AYLEDIPGLKDGKHPAISHRDIKSKVLLKNNLTACIADFGALKEAGKSGADTHGOV 360  
 |||||||  
 Db 301 AYLEDIPGLKDGKHPAISHRDIKSKVLLKNNLTACIADFGALKEAGKSGADTHGOV 360  
 |||||||  
 Qy 361 GTRYMAPEVLEGAINFORDAFLRDMYAGLVWELASRCTAADGVPDVEYMLPFEEIG 420  
 |||||||  
 Db 361 GTRYMAPEVLEGAINFORDAFLRDMYAGLVWELASRCTAADGVPDVEYMLPFEEIG 420  
 |||||||  
 Qy 421 QHPSEDMEQVYVVKRPPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCGVGERIT 480  
 |||||||  
 Db 421 QHPSEDMEQVYVVKRPPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCGVGERIT 480  
 |||||||  
 Qy 481 QMORLTNIITTEDIVVTVMVTVNVDPPKESL 513  
 |||||||  
 Db 481 QMORLTNIITTEDIVVTVMVTVNVDPPKESL 513  
 |||||||

RESULT 4  
 AVR2\_BOVIN STANDARD; PRT; 513 AA.  
 ID AVR2\_BOVIN  
 AC Q28043;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Activin receptor type II precursor (EC 2.7.1.37) (ACTR-II).  
 GN ACVR2 OR ACTRII.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Holstein; TISSUE=Testis;  
 RA MEDLINE=95203477; PubMed=7534730;  
 RX Ethier J.F., Houde A., Lussier J.G., Silversides D.W.;  
 RT "Bovine activin receptor type II cDNA: cloning and tissue  
 expression.";  
 RL Mol. Cell. Endocrinol. 106:1-8(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovary;  
 RX MEDLINE=97032546; PubMed=8875905;  
 RA Montegudo L.V., Heriz A., Flavin N., Rogers M., Ennis S.,  
 RA Arruga M.V.;  
 RT "Fluorescent in situ localization of the bovine activin receptor type  
 IIA locus on chromosome 2 (2q2.3-2.4).";  
 RL Mamm. Genome 7:869-869(1996).  
 CC -|- FUNCTION: RECEPTOR FOR ACTIVIN A, ACTIVIN B, AND INHIBIN A.  
 CC INVOLVED IN TRANSMEMBRANE SIGNALING.  
 CC -|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -|- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC TGF $\beta$  RECEPTOR SUBFAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; L21717; AAA74597.1; -;  
 CC EMBL; U43208; AAC48694.1; -;  
 CC HSSP; P27038; 1BTE.  
 CC InterPro; IPR000472; Activin\_rec.  
 CC InterPro; IPR000333; Actn\_receptorII.  
 CC InterPro; IPR000719; Euk\_pkinase.  
 CC InterPro; IPR002290; Ser\_thr\_pkinase.  
 CC Pfam; PF00069; pkinase; 1.  
 CC Pfam; PF01064; Activin\_recp; 1.  
 CC PRINTS; PR00653; ACTIVIN2R.

Dr ProDom; PD000001; Euk\_pkinase; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 KW Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding;  
 KW Transmembrane; Glycoprotein; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 513  
 FT DOMAIN 20 135  
 FT EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 136 161  
 FT DOMAIN 162 513  
 FT CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 192 485  
 FT PROTEIN KINASE.  
 FT NP\_BIND 198 206  
 FT BINDING 219 219  
 FT ACT\_SITE 322 322  
 FT BY SIMILARITY.  
 FT ACT\_SITE 43 43  
 FT CARBOHYD 66 66  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 66 66  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 513 AA; 57951 MW; C2969A54CF00617B CRC64;

Query Match 99.0%; Score 2743; DB 1; Length 513;  
 Best Local Similarity 98.4%; Pred. No. 1.2e-197;  
 Matches 505; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGAALKAFVAVFLISCGAIIIGRSETQCLFFFNANWEKDRNTGTGVEPCYGDKRRHC 60  
 |||||||  
 Db 1 MGAALKAFVAVFLISCGAIIIGRSETQCLFFFNANWEKDRNTGTGVEPCYGDKRRHC 60  
 |||||||  
 Qy 61 FATWKNISGIEIVKQGCWLDINDYDRTDCVEKKDSPEVYFCCCEGNNMCNEKFSYFPEM 120  
 |||||||  
 Db 61 FATWKNISGIEIVKQGCWLDINDYDRTDCVEKKDSPEVYFCCCEGNNMCNEKFSYFPEM 120  
 |||||||  
 Qy 121 EVTQPTSNEVTPKPPYNYLLSLVPLMLIAGIVICAFWVYRHHKMAPVLPVPTQDPGP 180  
 |||||||  
 Db 121 EVTQPTSNEVTPKPPYNYLLSLVPLMLIAGIVICAFWVYRHHKMAPVLPVPTQDPGP 180  
 |||||||  
 Qy 181 PPSPLLGKPLQLLEVKARGFGCVKQAQLNVEYVAVKIFPIQDKSQWNEYEYVSLPG 240  
 |||||||  
 Db 181 PPSPLLGKPLQLLEVKARGFGCVKQAQLNVEYVAVKIFPIQDKSQWNEYEYVSLPG 240  
 |||||||  
 Qy 241 MKHENILQFIGAEKRGTSVDVLDLWLTAFHEKGSLSDFLKANVWSNQLCHTAETMARGL 300  
 |||||||  
 Db 241 MKHENILQFIGAEKRGTSVDVLDLWLTAFHEKGSLSDFLKANVWSNQLCHTAETMARGL 300  
 |||||||  
 Qy 301 AYLEDIPGLKDGKHPAISHRDIKSKVLLKNNLTACIADFGALKEAGKSGADTHGOV 360  
 |||||||  
 Db 301 AYLEDIPGLKDGKHPAISHRDIKSKVLLKNNLTACIADFGALKEAGKSGADTHGOV 360  
 |||||||  
 Qy 361 GTRYMAPEVLEGAINFORDAFLRDMYAGLVWELASRCTAADGVPDVEYMLPFEEIG 420  
 |||||||  
 Db 361 GTRYMAPEVLEGAINFORDAFLRDMYAGLVWELASRCTAADGVPDVEYMLPFEEIG 420  
 |||||||  
 Qy 421 QHPSEDMEQVYVVKRPPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCGVGERIT 480  
 |||||||  
 Db 421 QHPSEDMEQVYVVKRPPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCGVGERIT 480  
 |||||||

RESULT 5  
 AVR2\_SHEEP STANDARD; PRT; 513 AA.  
 ID AVR2\_SHEEP  
 AC Q28560;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Activin receptor type II precursor (EC 2.7.1.37) (ACTR-II).  
 GN ACVR2 OR ACTRII.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;  
 OC Bovidae; Caprinae; Ovis.



```
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Romey; TISSUE=Ovarian follicle;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RC Tisdall D.J.;
CC -!- FUNCTION: RECEPTOR FOR ACTIVIN A, ACTIVIN B, AND INHIBIN A.
CC INVOLVED IN TRANSMEMBRANE SIGNALING.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC TGFB RECEPTOR SUBFAMILY.
CC -----
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CC -----
CC EMBL; LI9442; AAA91903.1; -
CC HSP; P27038; 1BTE.
CC InterPro: IPR000472; Activin_rec.
CC InterPro: IPR000333; Actn_receptorII.
CC InterPro: IPR000719; Euk_pkinase.
CC InterPro: IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; pkinase; 1.
CC Pfam; PF01064; Activin_rec; 1.
CC PRINTS; PR00653; ACTIVIN2R.
CC ProDom; PD000001; Euk_pkinase; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
CC Receptor; Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 513 ACTIVIN RECEPTOR TYPE II.
FT DOMAIN 20 135 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 136 161 POTENTIAL.
FT DOMAIN 162 513 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 192 485 PROTEIN KINASE.
FT NP_BIND 198 206 ATP (BY SIMILARITY).
FT BINDING 219 219 ATP (BY SIMILARITY).
FT ACT_SITE 322 322 BY SIMILARITY.
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 513 AA; 57768 MW; 7231BF9E85CA57E3 CRC64;

Query Match 97.6%; Score 2704; DB 1; Length 513;
Best Local Similarity 97.1%; Pred. No. 1e-194;
Matches 498; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 MGAALAFVFLISCSGAILGRSETQCLFFNANWEKDRNTQTCVPCYGDOKRRHC 60
DB 1 MGAALAFVFLISCSGAILGRSETQCLFFNANWEKDRNTQTCVPCYGDOKRRHC 60
QY 61 FATWKNISGIEIVKGGCGLDDINCVDYRDCVEKDSPEVYFCCEGNNCNEKFSYFPEM 120
DB 61 FATWKNISGIEIVKGGCGLDDINCVDYRDCVEKDSPEVYFCCEGNNCNEKFSYFPEM 120
QY 121 EVTQPTSNVTPKPPYNYLLSLVPLMLIAGIVCAFVYRHHKMAYPVLPVPTQDPGP 180
DB 121 EVTQPTSNVTPKPPYNYLLSLVPLMLIAGIVCAFVYRHHKMAYPVLPVPTQDPGP 180
QY 181 PPSPLGLKPLQLLEVKARGGCVWKAQLLNEYAVKFIQDKSQHNEYEYVSLPG 240
DB 181 PPSPLGLKPLQLLEVKARGGCVWKAQLLNEYAVKFIQDKSQHNEYEYVSLPG 240
QY 241 MKHENILOFIGAEGKRTSDVDLWLTITAFHEKGSLSDFLKANVSNWOLCHIAETMARGL 300
DB 241 MKHENILOFIGAEGKRTSDVDLWLTITAFHEKGSLSDFLKANVSNWOLCHIAETMARGL 300
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QY 301 AYLHEDIPLGDKHKAIPASHRDIKSNVLLKNNLTACIADFGALKFEAGKSAGDTHGOV 360
DB 301 AYLHEDIPLGDKHKAIPASHRDIKSNVLLKNNLTACIADFGALKFEAGKSAGDTHGOV 360
QY 361 GTRRYMAPEVLEGAINFORDAFRLIDMYAGLVWLWELASRCTAADGPVDEYMLPFEEIG 420
DB 361 GTRRYMAPEVLEGAINFORDAFRLIDMYAGLVWLWELASRCTAADGPVDEYMLPFEEIG 420
QY 421 QHPSLEDQEVVVVHKRPVLDYQKHAGMAMLCETEECWHDHAEARLSAGCVGERIT 480
DB 421 QHPSLEDQEVVVVHKRPVLDYQKHAGMAMLCETEECWHDHAEARLSAGCVGERIT 480
QY 481 QMQRLTNIITIEDIVVTVMVTNVDFPKKESL 513
DB 481 QMQRLTNIITIEDIVVTVMVTNVDFPKKESL 513

RESULT 6
AVR2_XENLA STANDARD; PRT; 514 AA.
ID AC P27039;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Activin receptor type II precursor (EC 2.7.1.37) (ACTR-II).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9205974; PubMed=1661587;
RA Kondo M., Tashiro K., Fujii G., Asano M., Miyoshi R., Yamada R.,
RA Muramatsu M., Shiohawa K.;
RT "Activin receptor mRNA is expressed early in Xenopus embryogenesis
RT and the level of the expression affects the body axis formation.";
RL Biochem. Biophys. Res. Commun. 181:684-690(1991).
CC -!- FUNCTION: RECEPTOR FOR ACTIVIN A, ACTIVIN B, AND INHIBIN A.
CC INVOLVED IN TRANSMEMBRANE SIGNALING.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC TGFB RECEPTOR SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; S70930; AAB20638.1; -
CC PIR; JQ1317; JQ1317.
CC HSP; P27038; 1BTE.
CC InterPro: IPR000472; Activin_rec.
CC InterPro: IPR000333; Actn_receptorII.
CC InterPro: IPR000719; Euk_pkinase.
CC InterPro: IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; pkinase; 1.
CC Pfam; PF01064; Activin_rec; 1.
CC PRINTS; PR00653; ACTIVIN2R.
CC ProDom; PD000001; Euk_pkinase; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
CC Receptor; Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 20
FT CHAIN 21 514 ACTIVIN RECEPTOR TYPE II.
FT DOMAIN 21 136 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 137 162 POTENTIAL.
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QY 419 IGOHPSLEDQVWVHHKRPVLRDQWQKHAGMAMLCETIEECWDHDAEARLSAGCVGER 478
Db 417 IGOHPSLEDQVWVHHKRPVLRDQWQKHAGMAMLCETIEECWDHDAEARLSAGCVGER 476
QY 479 ITOMORLTNIITIEDIVVTWMTNVDFPPKESL 513
Db 477 ISQIRSVNGETSDCLVSVITVNTVDLPKESSI 511

RESULT 8
ID AVRB_HUMAN STANDARD; PRT; 512 AA.
AC Q13705;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Activin receptor type IIB precursor (EC 2.7.1.37) (ACTR-IIB).
EN ACVR2B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=94214127; PubMed=8161782;
RX Hilden K., Tuuri T., Eramaa M., Ritvos O.;
RT "Expression of type II activin receptor genes during differentiation
RT of human K562 cells and cDNA cloning of the human type IIB activin
RT receptor.";
RL Blood 83:2163-2170(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98284539; PubMed=9621519;
RA Ishikawa S., Kai M., Murata Y., Tamari M., Daigo Y., Murano T.,
RA Ogawa M., Nakamura Y.;
RT "Genomic organization and mapping of the human activin receptor type
RT IIB (hActr-IIB) gene.";
RL J. Hum. Genet. 43:132-134(1998).
RN [3]
RP SEQUENCE FROM N.A.; ALTERNATIVE SPLICING, AND VARIANTS LR AXIS
RX MALFORMATIONS HIS-40 AND ILE-454.
RX MEDLINE=99113885; PubMed=9916847;
RA Kosaki R., Gebbia M., Kosaki K., Lewin M., Bowers P., Towbin J.A.,
RA Casey B.;
RT "Left-right axis malformations associated with mutations in ACVR2B,
RT the gene for human activin receptor type IIB.";
RL Am. J. Med. Genet. 82:70-76(1999).
CC -! FUNCTION: RECEPTOR FOR ACTIVIN A, ACTIVIN B AND INHIBIN A.
CC INVOLVED IN TRANSMEMBRANE SIGNALING.
CC -! CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -! SUBCELLULAR LOCATION: Type I membrane protein.
CC -! ALTERNATIVE PRODUCTS: 2 isoforms: ACTR-IIB1 and ACTR-IIB2 (shown
CC here); may be produced by alternative splicing. ACTR-IIB1 results
CC from the insertion in the transcript of 82 base pairs, leading to
CC frameshift and protein truncation. It is not known whether or not
CC ACTR-IIB1 has any biological function.
CC -! DISEASE: Defects in ACVR2B are a cause of left-right (LR) axis
CC malformations, due to the loss of normal left-right asymmetry.
CC Complete left-right asymmetry reversal imparts no deleterious
CC consequences to the affected individual, whereas randomization
CC typically results in complex, often lethal heart malformations as
CC well as abdominal abnormalities.
CC -! SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC TGFB RECEPTOR SUBFAMILY.

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CC EMBL; X77533; CRA54671.1; -
DR EMBL; AB008681; DAA24180.2; -
DR EMBL; AF060202; AAC64515.1; -
DR EMBL; AF060199; AAC64515.1; JOINED.
DR EMBL; AF060200; AAC64515.1; JOINED.
DR EMBL; AF060201; AAC64515.1; JOINED.
DR HSSP; P27038; 1BPE.
DR Genew; HGNC:174; ACVR2B.
DR MIM; 602730; -
DR InterPro; IPR000472; Activin_rec.
DR InterPro; IPR000333; Actn_receptorII.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF01064; Activin_rec; 1.
DR PRINTS; PR00653; ACTIVIN2R.
DR PRODOM; PD000001; Euk_pkinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Receptor; transferase; Serine/threonine-protein kinase; ATP-binding;
KW Transmembrane; Glycoprotein; Signal; Disease mutation;
KW Alternative splicing.
FT SIGNAL 1 18
FT CHAIN 19 512
FT DOMAIN 19 134
FT TRANSMEM 135 160
FT DOMAIN 161 512
FT DOMAIN 190 480
FT NP_BIND 196 204
FT BINDING 217 217
FT ACT_SITE 321 321
FT CARBOHYD 42 42
FT CARBOHYD 65 65
FT VARIANT 40 40
FT VARIANT 494 494
FT CONFLICT 16 17
FT CONFLICT 64 64
FT CONFLICT 459 459
FT CONFLICT 459 459
SQ SEQUENCE 512 AA; 57638 MW; 13E3225073E229A3 CRC64;

Query Match 70.28; Score 1944; DB 1; Length 512;
Best Local Similarity 67.3%; Pred. No. 6.2e-138;
Matches 342; Conservative 88; Mismatches 76; Indels 2; Gaps 2;

QY 7 LAFAVFLISCSGAILGRSETQECLEFFNANWEKDRITQTVGPECYGDKRRHCFATWKN 66
Db 6 VALALLWGLSCLAGSGRGAETRECIYNNANWELETRTQSLERCEGEQDRLHCHYASWAN 65
QY 67 IGSIEIVQCWLDDINCVDRTDCVEKKDSPEYVYFCCCEGNCMCNEKSFYFPEMEVTQPT 126
Db 66 SSGTIELWKGCLWDDFNCYDRQCVATEENPQVYFCCCEGNCNEFTLHPEAGGPEVT 125
QY 127 SNVTPPPYNNILYSIVPLMLTAGIVCAFVWYRHHKWAYPPVLYPTQDPGPPPSPL 186
Db 126 YEPPTAPTLLTULAYSLPLTGGUSLIVLAFWYRHRKPPYGHVDI-HEDPGPPPSPL 184
QY 187 LGLPLQLLEVKARGFCGVWKAQLLNEYVAVKIFPQDKQSQWONEYVYSLPMKHENI 246
Db 185 VGLPLQLLEIKARGFCGVWKAQLMNDFAVKIFPLQDKQSQWSEIREIFSTPMKHENL 244
QY 247 LQFICAKRGTSVDVLDLWLTAFHEKSLSDFLKANVVSNNQLCHTAETWARGLAYLHED 306
Db 245 LQFIAEKRGSLNVELWLITAFHDKSLFDYLNKNIITWNLCHVAETMSRGLSYLHED 304
QY 307 IPGLK-DGHPAISHRDIKSKNVLKNNLTACTADFGALKFEAGKSGAGTHQGVTRY 365
Db 305 VPCRGEGHPRSTIAHRDFKSKNVLKSDLTAVLADFLAVRFPKPPGPDTHQGVTRY 364

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Query Match 52.7%; Score 1460; DB 1; Length 382;
Best Local Similarity 68.9%; Pred. No. 6.4e-102;
Matches 264; Conservative 62; Mismatches 55; Indels 2; Gaps 2;

Qy 116 YPPEVETPTSPNPTPKPPYNTLLSLVPLMLIAGIVICAFWYRHHKMYPPVLPVT 175
Db 1 HLPEFGPEVTPPTAPTLLTTLAYSLPLIGGLSLIVLLAFWYRHHKPPYGHVDI-H 59

Qy 176 QDPGPPPSPLGLKPLQLLEVKARGFGCWKAQLNEXYVAVKFIQDKSQNQEYEV 235
Db 60 EDGPPPPSPLVGLKPLQLLEIKARGFGCWKAQLNDFVAVKFIQDKSQNQSREI 119

Qy 236 YSLPGMKHENTLQITGAERKGTSDVDLWLITAFHEKGSLSDFLKNVSNWLCHTAET 295
Db 120 FSTPGMKHENTLQITGAERKGTSDVDLWLITAFHEKGSLSDFLKNVSNWLCHVAET 179

Qy 296 MARGLAYLHEDIPLGL-DGHKPAISHRDIKSNVLLKNNLTACIADFGALKPEAGKSAG 354
Db 180 MSRGSLYLHEDVPMCRGEGHKPSIAHREFKSNVLLKNNLTAVLADFGAVRPEPGKPPG 239

Qy 355 DTHGOVGRTRRYMAPEVLEGAINFORDAFLRIDMYAMGLVLMELASRCTAADGPPVDEYMLP 414
Db 240 DTHGOVGRTRRYMAPEVLEGAINFORDAFLRIDMYAMGLVLMELWELVSRCKAAGPPVDEYMLP 299

Qy 415 FEEIGQHPSLDQEVVYVHKKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEARSAGC 474
Db 300 SEEEIGQHPSLDQEVVYVHKKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEARSAGC 359

Qy 475 VGERITQMTQNTIITTDIVTV 497
Db 360 VEVRSLIRSVNGSTSDCLVSL 382

RESULT 12
TGR2_MOUSE STANDARD; PRT; 592 AA.
AC Q62312; Q63947;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TGF-beta receptor type II precursor (EC 2.7.1.37) (TGF-beta
DE type II receptor).
GN TGFBR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain;
MEDLINE=95046367; PubMed=7957954;
SU Suzuki A., Shioda N., Maeda T., Tada M., Ueno N.;
RT "Cloning of an isoform of mouse TGF-beta type II receptor gene.";
RL FEBS Lett. 355:19-22(1994).
RN [2]
SEQUENCE FROM N.A.
RX MEDLINE=94163970; PubMed=8119124;
RA Lawler S., Candia A.F., Ebner R., Shum L., Lopez A.R., Moses H.L.,
RA Wright C.V., Derynck R.;
RT "The murine type II TGF-beta receptor has a coincident embryonic
RT expression and binding preference for TGF-beta 1.";
RL Development 120:165-175(1994).
CC - FUNCTION: TYPE I/TYPE II TGF-BETA RECEPTORS FORM AN HETEROMERIC
CC COMPLEX AFTER BINDING TGF-BETA AT THE CELL SURFACE AND ACT AS
CC SIGNAL TRANSDUCERS.
CC - CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC - SUBCELLULAR LOCATION: Type I membrane protein.
CC - ALTERNATIVE PRODUCTS: 2 ISOFORMS; RII-1 AND RII-2 (SHOWN HERE);
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC - TISSUE SPECIFICITY: WIDELY EXPRESSED IN ADULT. EXPRESSED PRIMARILY
CC IN MESENCHYME AND EPIDERMIS OF THE MIDGESTATIONAL FETUS.
CC - PTM: PHOSPHORYLATED ON A SER/THR RESIDUE IN THE CYTOPLASMIC
```



OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=92154690; PubMed=1310899;  
 RA Lin H.Y., Wang X.-F., Ng-Eaton E., Weinberg R.A., Lodish H.F.;  
 RT "Expression cloning of the TGF-beta type II receptor, a functional  
 transmembrane serine/threonine kinase.";  
 RL Cell 68:775-785(1992).  
 RN [2]  
 RP ERRATUM.  
 RA Lin H.Y., Wang X.-F., Ng-Eaton E., Weinberg R.A., Lodish H.F.;  
 RL Cell 70:1068-1068(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96411693; PubMed=8812462;  
 RA Takenoshita S., Hagiwara K., Nagashima M., Gemma A., Bennett W.P.,  
 Harris C.C.;  
 RT "The genomic structure of the gene encoding the human transforming  
 growth factor beta type II receptor (TGF-beta.RII).";  
 RL Genomics 36:341-344(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96438608; PubMed=8840968;  
 RA Lu S.L., Zhang W.C., Akiyama Y., Nomizu T., Yuasa Y.;  
 RT "Genomic structure of the transforming growth factor beta type II  
 receptor gene and its mutations in hereditary nonpolyposis colorectal  
 cancers.";  
 RL Cancer Res. 56:4595-4598(1996).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=97128789; PubMed=8973329;  
 RA Ogasa H., Noma T., Murata H., Kawai S., Nakazawa A.;  
 RT "Cloning of a cDNA encoding the human transforming growth factor-beta  
 type II receptor: heterogeneity of the mRNA.";  
 RL Gene 181:185-190(1996).  
 RN [6]  
 RP VARIANT HNPCC MET-315.  
 RX MEDLINE=98250164; PubMed=9590282;  
 RA Lu S.-L., Kawabata M., Imamura T., Akiyama Y., Nomizu T., Miyazono K.,  
 Yuasa Y.;  
 RT "HNPCC associated with germline mutation in the TGF-beta type II  
 receptor gene.";  
 RL Nat. Genet. 19:17-18(1998).  
 CC -!- FUNCTION: TYPE I/TYPE II TGF-BETA RECEPTORS FORM AN HETEROMERIC  
 COMPLEX AFTER BINDING TGF-BETA AT THE CELL SURFACE AND ACT AS  
 SIGNAL TRANSDUCERS.  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated protein.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- PTM: PHOSPHORYLATED ON A SER/THR RESIDUE IN THE CYTOPLASMIC  
 DOMAIN.  
 CC -!- DISEASE: DEFECTS IN TGFBR2 ARE THE CAUSE OF HEREDITARY  
 NONPOLYPOSIS COLORECTAL CANCER (HNPCC).  
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC TGF RECEPTOR SUBFAMILY.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; M85079; AAB61164.1; -;  
 DR EMBL; U52246; AAB17553.1; -;  
 DR EMBL; U52240; AAB17553.1; JOINED.  
 DR EMBL; U52241; AAB17553.1; JOINED.  
 DR EMBL; U52242; AAB17553.1; JOINED.  
 DR EMBL; U52244; AAB17553.1; JOINED.

DR EMBL; U52245; AAB17553.1; JOINED.  
 DR EMBL; U69152; AAB40916.1; -;  
 DR EMBL; U69146; AAB40916.1; JOINED.  
 DR EMBL; U69147; AAB40916.1; JOINED.  
 DR EMBL; U69148; AAB40916.1; JOINED.  
 DR EMBL; U69149; AAB40916.1; JOINED.  
 DR EMBL; U69150; AAB40916.1; JOINED.  
 DR EMBL; U69151; AAB40916.1; JOINED.  
 DR EMBL; U50683; BAA09332.1; -;  
 DR PIR; A42100; A42100.  
 DR Genew; HGNC:11773; TGFBR2.  
 DR MIM; 190182; -;  
 DR InterPro; IPR000472; Activin\_rec.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000001; Euk\_pkinase; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding;  
 KW Transmembrane; Phosphorylation; Glycoprotein; Signal;  
 KW Disease mutation.  
 FT SIGNAL 1 23 POTENTIAL.  
 FT CHAIN 24 567 TGF-BETA RECEPTOR TYPE II.  
 FT DOMAIN 24 166 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 167 187 POTENTIAL.  
 FT DOMAIN 188 567 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 244 544 PROTEIN KINASE.  
 FT NP\_BIND 250 258 ATP (BY SIMILARITY).  
 FT BINDING 277 277 ATP (BY SIMILARITY).  
 FT ACT\_SITE 379 379 BY SIMILARITY.  
 FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 94 94 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARIANT 315 315 T -> M (IN HNPCC).  
 FT CONFLICT 381 381 /FTID=VAR\_008156.  
 FT SEQUENCE 567 AA; 64539 MW; C8DAC5651FFBC4FB CRC64;  
 SQ  
 Query Match 28.0%; Score 775.5; DB 1; Length 567;  
 Best Local Similarity 35.6%; Pred. No. 1.4e-50;  
 Matches 176; Conservative 82; Mismatches 140; Indels 97; Gaps 15;  
 QY 60 CFATWKNISGSIIVKOGCWLDDINDYD-----ETVCHDPKLPYHDFILEDAAAPKIMKEKKPGTFFM 135  
 DB 84 CVAVWRKNDENITL-----ETVCHDPKLPYHDFILEDAAAPKIMKEKKPGTFFM 135  
 QY 103 CCCEGNMCNEKFSYFPFEMEVTQPTSNPTPKPPYYNILL-----YSLVPLMLIAGIVI 155  
 DB 136 CSCSDECDNDNIIFSEYN-----TSNP-----DLLLVIFQVTGISLPLGLVAISVI 183  
 QY 156 CAFWVVRHKKMAYPPVLPVTPQDPGPPPP-----SPLLG 188  
 DB 184 IIFCYRVNRQ---QKLSSTWETGTRKLMFSEHCAIILEDSDRSISSTCANNHNTE 240  
 QY 189 LKPLQLLEVKARGFGCVKQAQLN-----EYVAVKIFPIQDKQSWQNEYEYVSLPGMK 242  
 DB 241 LLPIELDTLVKGRAEYVKAKLKQNTSEQFETVAVKIFPEYEAWSKTEKDFISDINK 300  
 QY 243 HENILOFIGNKRGTSVDVLDLITAFHEKGSLSDFLKNVYVSNOLCHIAETMARGLAY 302  
 DB 301 HENILOFLTAERKTELGKQYWLITAFHAKGNLQYELTRHVISWEDRLKGLSGLANGIAH 360  
 QY 303 LHEDIPLGLKDGHPA-----ISHRDIKSNVLLKNNLTACIADFGLALKFEAGSAGD- 355  
 DB 361 LHSD-----HTPCGPRKMPIVHRDLKSSNLTILKNDLTCCCLCDFGLSLRDLPTLSVDL 413  
 QY 356 -THQGVQTRRYMAPEVLEGAINPQR-DAFLRDMYAMGLVLMELASRCRTAAGPVDVEYML 413  
 DB 414 ANSGQVGTARYMAPEVLESRMNLNAESFKQTDVYSWALVLMELTSCNAV-GEVKDYEP 472  
 QY 414 PFEEIIGQHPLESMDQEVVVHKKRPVLDYQWKHAGMAWLCETIECDHDAEARLSAG 473



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Db 473 PFSGKYREHPCVSMKDNVLRGRPEIPSWLHOGIOMVCEITLQWHDPEARLTAQ 532
QY 474 CVGERITOMORLTNI 488
Db 533 CVAERFSELEHDLRL 547

RESULT 15
BMR2_HUMAN
ID BMR2_HUMAN STANDARD; PRT; 1038 AA.
AC Q13873; Q16569;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Bone morphogenetic protein receptor type II precursor (EC 2.7.1.37)
DE Bone morphogenetic protein receptor type II precursor (EC 2.7.1.37)
DE (BMP type II receptor) (BMPR-II).
DE BMR2 OR PPH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Substantia nigra;
RX MEDLINE=95372334; PubMed=7644468;
RA Rosenzweig B.L., Imamura T., Okadome T., Cox G.N., Yamashita H.,
RA ten Dijke P., Heldin C., Miyazono K.;
RT "Cloning and characterization of a human type II receptor for bone
RT morphogenetic proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:7632-7636(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin fibroblast;
RX MEDLINE=95403457; PubMed=7673243;
RA Nohno T., Ishikawa T., Saito T., Hosokawa K., Noji S., Wosing D.H.,
RA Rosenbaum J.S.;
RT "Identification of a human type II receptor for bone morphogenetic
RT protein-4 that forms differential heteromeric complexes with bone
RT morphogenetic protein type I receptors.";
RL J. Biol. Chem. 270:22522-22526(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95197572; PubMed=7890663;
RA Kawabata M., Chytil A., Moses H.L.;
RT "Cloning of a novel type II serine/threonine kinase receptor through
RT interaction with the type I transforming growth factor-beta
RT receptor.";
RL J. Biol. Chem. 270:5625-5630(1995).
RN [4]
RP VARIANTS PPH GLN-491 AND TRP-491.
RX PubMed=10903931;
RA Deng Z., Morse J.H., Slager S.L., Cuervo N., Moore K.J., Venetos G.,
RA Kalachikov S., Cayanis E., Fischer S.G., Barst R.J., Hodge S.E.,
RA Knowles J.A.;
RT "Familial primary pulmonary hypertension (gene PPH1) is caused by
RT mutations in the bone morphogenetic protein receptor-II gene.";
RL Am. J. Hum. Genet. 67:737-744(2000).
RN [5]
RP VARIANTS PPH TYR-60; TYR-117 AND ARG-483.
RX PubMed=11015450;
RA Thomson J.R., Machado R.D., Pauculo M.W., Morgan N.V., Humbert M.,
RA Elliott G.C., Ward K., Yacoub M., Mikhail G., Rogers P., Newman J.H.,
RA Wheeler L., Higenbottam T., Gibbs J.S.R., Egan J., Crozier A.,
RA Peacock A., Allcock R., Corris P., Loyd J.E., Trembath R.C.,
RA Nichols W.C.;
RT "Sporadic primary pulmonary hypertension is associated with germline
RT mutations of the gene encoding BMPR-II, a receptor member of the
RT TGF-beta family.";
RL J. Med. Genet. 37:741-745(2000).
RN [6]
RP VARIANTS PPH TRP-118; TYR-347 AND GLY-485.
RX PubMed=10973254;

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RA Lane K.B., Machado R.D., Pauculo M.W., Thomson J.R.,
RA Phillips J.A. III, Loyd J.E., Nichols W.C., Trembath R.C., Aldred M.,
RA Brannon C.A., Conneally P.M., Foroud T., Fretwell N., Gaddipati R.,
RA Koller D., Loyd E.J., Morgan N.V., Newman J.H., Prince M.A.,
RA Villarino Gueell C., Wheeler L.;
RA "Heterozygous germline mutations in BMPR2, encoding a TGF-beta
RA receptor, cause familial primary pulmonary hypertension.";
RL Nat. Genet. 26:81-84(2000).
RN [7]
RP VARIANTS PPH ARG-123; SER-123; ARG-420 AND THR-512, VARIANT ASP-224,
RP AND CHARACTERIZATION OF VARIANT PPH GLY-485.
RX PubMed=11115378;
RA Machado R.D., Pauculo M.W., Thomson J.R., Lane K.B., Morgan N.V.,
RA Wheeler L., Phillips J.A. III, Newman J.H., Williams D., Galie N.,
RA Manes A., McNeil K., Yacoub M., Mikhail G., Rogers P., Corris P.,
RA Humbert M., Donnai D., Martensson G., Tranebjaerg L., Loyd J.E.,
RA Trembath R.C., Nichols W.C.;
RA "BMPR2 haploinsufficiency as the inherited molecular mechanism for
RA primary pulmonary hypertension.";
RL Am. J. Hum. Genet. 68:92-102(2001).
CC -1- FUNCTION: BINDS TO BMP-7, BMP-2 AND, LESS EFFICIENTLY, BMP-4.
CC BINDING IS WEAK BUT ENHANCED BY THE PRESENCE OF TYPE I RECEPTORS
CC FOR BMPs.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBUNIT: HETERODIMERIZE WITH TYPE-I RECEPTORS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART AND LIVER.
CC -1- DISEASE: Defects in BMPR2 are the cause of primary pulmonary
CC hypertension (PPH), a rare autosomal dominant disorder
CC characterized by pleomorphic lesions of proliferating endothelial
CC cells in pulmonary arterioles. The lesions lead to elevated
CC pulmonary arterial pressure, right ventricular failure, and death.
CC The disease can occur from infancy throughout life and it has a
CC mean age at onset of 36 years. Penetrance is reduced. Although
CC familial PPH is rare, cases secondary to known etiologies are more
CC common and include those associated with the appetite-suppressant
CC drugs.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC TGFb RECEPTOR SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z48923; CAA88759.1; -.
CC EMBL; D50516; BAA09094.1; -.
CC EMBL; U20165; AAC50105.1; -.
CC Genew; HGNC:1078; BMPR2.
CC MIM; 600799; -.
CC MIM; 178600; -.
CC InterPro; IPR000472; Activin_rec.
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; pkinase; 1.
CC Pfam; PF01064; Activin_rec; 1.
CC Prodom; PD000001; Euk_pkinase; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
CC PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
CC Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding;
CC Transmembrane; Glycoprotein; Signal; Polymorphism; Disease mutation.
CC SIGNAL 1 26 POTENTIAL.
CC CHAIN 27 1038 BONE MORPHOGENETIC PROTEIN RECEPTOR TYPE
CC II.
CC DOMAIN 27 150 EXTRACELLULAR (POTENTIAL).
CC TRANSEM 151 171 POTENTIAL.
CC DOMAIN 172 1038 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 203 504 PROTEIN KINASE.
CC NP_BIND 209 217 ATP (BY SIMILARITY).

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FT BINDING 230 230 ATP (BY SIMILARITY).
FT ACT_SITE 333 333 BY SIMILARITY.
FT DOMAIN 547 550 POLY-SER.
FT DOMAIN 610 618 POLY-THR.
FT DOMAIN 901 908 POLY-ASN.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 126 126 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 60 60 C -> Y (IN PPH).
FT VARIANT 117 117 /FTid=VAR_013670.
FT VARIANT 117 117 C -> Y (IN PPH).
FT VARIANT 118 118 /FTid=VAR_013671.
FT VARIANT 118 118 C -> W (IN PPH).
FT VARIANT 123 123 /FTid=VAR_013672.
FT VARIANT 123 123 C -> R (IN PPH).
FT VARIANT 123 123 /FTid=VAR_013673.
FT VARIANT 123 123 C -> S (IN PPH).
FT VARIANT 224 224 /FTid=VAR_013674.
FT VARIANT 224 224 E -> D.
FT VARIANT 347 347 /FTid=VAR_013675.
FT VARIANT 347 347 C -> Y (IN PPH).
FT VARIANT 420 420 /FTid=VAR_013676.
FT VARIANT 420 420 C -> R (IN PPH).
FT VARIANT 483 483 /FTid=VAR_013677.
FT VARIANT 483 483 C -> R (IN PPH; SPORADIC).
FT VARIANT 485 485 /FTid=VAR_013678.
FT VARIANT 485 485 D -> G (IN PPH; COMPLETE LOSS OF
FUNCTION).
FT VARIANT 491 491 /FTid=VAR_013679.
FT VARIANT 491 491 R -> Q (IN PPH; SPORADIC).
FT VARIANT 491 491 /FTid=VAR_013680.
FT VARIANT 491 491 R -> W (IN PPH).
FT VARIANT 512 512 /FTid=VAR_013681.
FT VARIANT 512 512 K -> T (IN PPH).
FT VARIANT 519 519 /FTid=VAR_013682.
FT VARIANT 519 519 N -> K (IN PPH).
FT VARIANT 828 828 /FTid=VAR_013683.
FT CONFLICT 828 828 G -> R (IN REF.1).
FT SEQUENCE 1038 AA; 115201 MW; 1389923CE574B913 CRC64;

Query Match 28.0%; Score 775.5; DB 1; Length 1038;
Best Local Similarity 34.5%; Pred. No. 2.9e-50;
Matches 179; Conservative 103; Mismatches 172; Indels 65; Gaps 19;

Qy 7 LAFVFLISCSGAILGRSETQCL-EFFNANWEKDR-----TNQTGVEPCYCDKDKRR 58
Db 14 LPWILLVSTAA-----SQNERLCAFKDPYQODLIGESRISHENGITLC-----SKGS 64

Qy 59 HCFATWKNISGIEIVKQGCWL---DDINCYDRDVCVEKKDSEVY-----FCCCEGNMC 110
Db 65 TCYGLWEKSKGIDNLVKQGCWSHIGDPQECH-YEECVVTTTPPSIQNGTYRFCCCSIDL 123

111 NEKFS-YFPENEVTQPTSNVTPKPPYNN---ILLYSLVPLMLIAGIVICAFWVYRHHKM 166
124 NVNTEFP-----PPDTPLSP-PHSFNDETIILALASVSLAVLVALVCFGYR---- 173

Qy 167 AYPVLPVTPDGP-----PPPPSPLLGLKPLQLLEVKARGFCGKWKQAQLLNEYVAV 218
Db 174 ---MLTGDRKQGLHSMNMEAAASEPSLDDNLKLLLELIGRGYGYVYKGS�DERPVAV 229.

Qy 219 KIFPIQDKQSQWNEYVYSLPGMKHENILOFIAEKRGTSVD-VDLWLITAFHEKGSLSLD 277
Db 230 KVFSEFANRQNP INEKNIYRVPMEHDNIARFIVGDERVTADGRMEYLLVMVEYYPNGSLCK 289

Qy 278 FLKANVYSWNLCHIAETMARGLAYLHEDIPGLKDGHPALSHRDIKSKNVLKNNLTAC 337
Db 290 YLSLTSDWSSCRLAHSVTRGLAYLTLP-RGDHYKPAISHRDLSNRNVLKNDGTCV 348

Qy 338 IADFGALAKF-----EAGKSAGTHQGVGTRRYMAPEVLEGAINFQ--RDAFLRIDMYA 389
Db 349 ISDFGLSMRLGNLRVPGEDNAAISEVGTIRYMAPEVLEGAVNLRCESALKQVDMYA 408

Qy 390 MGLVLWELASRCT--AADGPVDEMLPFEIEIGQHPLESMDQEVVVHKKRPVLRDYNQK 447
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Db 409 LGLIYWEIFMRCTDLFPGESVPEYQMAFQTEVGNHPTFEDMQVLVSREKQRPKFPPEANKE 468
Qy 448 HA-GMAMLCETIEECWDHDAEARLSAGCVGERITOMORL 485
Db 469 NSLAVRSLKETIEDCDWDQDAEARLTAQCAERMAELMMI 507

Search completed: May 10, 2003, 18:07:08
Job time : 29 secs
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